

Hale, Mary

10/27 01

From: Ulm, John
Sent: Wednesday, October 22, 2003 3:36 PM
To: Hale, Mary
Subject: RE: problem with search request for SN 09/851,494

OK, let's modify the search. I need a search of nucleotides 5500 to 7000 and 9000 to 9200 of SEQ ID NO:1, which contain specifically claimed diagnostic mutations outside of a coding region, as well as nucleotides 400 to 1500 of SEQ ID NO:2, which appears to be a coding region within SEQ ID NO:1 and which contains seven additional diagnostic mutations. If this presents a problem, I can divide SEQ ID NO:2 into fragments containing the specifically recited mutations.

-----Original Message-----

From: Hale, Mary
Sent: Tuesday, October 21, 2003 3:46 PM
To: Ulm, John
Cc: Martinell, James
Subject: RE: problem with search request for SN 09/851,494
Importance: High

per attached note

Ulm
10/22/03

~~cancel~~
~~ixm contacted 10/21~~

(3110)

OCT 21 2003

RECEIVED

10/22/03
Ulm

LB 1-13,270 no → per attached note
3-580 aa
per ixm

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr.Link _____
Date Completed: _____	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 27, 2003, 18:04:00 ; Search time 441 Seconds
(without alignments)
220.243 Million cell updates/sec

Title: US-09-851-494B-3

Perfect score: 3067

Sequence: 1 MTAPAGRGSETERLLTPNP.....CSLLCCGRDPSEHSLLVN 580

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3067	100.0	580	9	US-09-828-466-2
2	3067	100.0	580	10	US-09-965-529-13
3	3067	100.0	580	11	US-09-965-529-13
4	3067	100.0	580	14	US-10-103-458-2
5	2665	86.9	511	9	US-09-820-893-63
6	1376	44.9	538	12	US-10-114-153-26
7	1368	44.6	566	12	US-10-114-153-28
8	1367	44.6	544	12	US-10-114-153-24
9	1314	42.8	540	12	US-10-114-153-22
10	1226	40.0	255	11	US-09-866-050A-713
11	689	22.5	193	11	US-09-796-753-162
12	281.5	9.2	69	9	US-09-864-761-45089
13	152.5	5.0	621	14	US-10-005-211-2
14	152.5	5.0	966	9	US-09-828-466-6
15	150.5	4.9	76	9	US-09-864-761-41295

16	141.5	4.6	224	9	US-09-864-761-48727	Sequence 48727, A
17	139.5	4.5	179	12	US-10-029-386-32155	Sequence 32155, A
18	138	4.5	866	9	US-09-753-008-1	Sequence 1, Appli
19	127	4.1	53	9	US-09-864-761-44873	Sequence 44873, A
20	127	4.1	968	9	US-09-753-008-7	Sequence 7, Appli
21	123	4.0	724	10	US-09-796-720B-5	Sequence 5, Appli
22	123	4.0	724	12	US-10-146-733-25	Sequence 25, Appl
23	113	3.7	49	9	US-09-864-761-44699	Sequence 44699, A
24	106.5	3.5	1447	10	US-09-808-571A-2	Sequence 2, Appli
25	101	3.3	323	15	US-10-288-160-12	Sequence 12, Appl
26	100	3.3	886	12	US-10-199-672-524	Sequence 524, App
27	100	3.3	886	12	US-10-187-749-524	Sequence 524, App
28	100	3.3	886	12	US-10-194-457-524	Sequence 524, App
29	100	3.3	886	12	US-10-184-642-524	Sequence 524, App
30	100	3.3	886	12	US-10-196-747-524	Sequence 524, App
31	100	3.3	886	12	US-10-173-689-524	Sequence 524, App
32	100	3.3	886	12	US-10-173-690-524	Sequence 524, App
33	100	3.3	886	12	US-10-173-691-524	Sequence 524, App
34	100	3.3	886	12	US-10-173-692-524	Sequence 524, App
35	100	3.3	886	12	US-10-173-694-524	Sequence 524, App
36	100	3.3	886	12	US-10-173-698-524	Sequence 524, App
37	100	3.3	886	12	US-10-173-699-524	Sequence 524, App
38	100	3.3	886	12	US-10-173-707-524	Sequence 524, App
39	100	3.3	886	12	US-10-174-569-524	Sequence 524, App
40	100	3.3	886	12	US-10-174-583-524	Sequence 524, App
41	100	3.3	886	12	US-10-174-587-524	Sequence 524, App
42	100	3.3	886	12	US-10-174-589-524	Sequence 524, App
43	100	3.3	886	12	US-10-174-591-524	Sequence 524, App
44	100	3.3	886	12	US-10-175-736-524	Sequence 524, App
45	100	3.3	886	12	US-10-175-742-524	Sequence 524, App

ALIGNMENTS

RESULT 1
US-09-828-466-2
; Sequence 2, Application US/09828466
; Patent No. US20020035056A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
; FILE REFERENCE: MNI-125CP
; CURRENT APPLICATION NUMBER: US/09/828,466
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/544,797
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-466-2

Query Match	100.0%	Score 3067;	DB 9;	Length 580;
Best Local Similarity	100.0%	Pred. No. 2.4e-289;		
Matches 580;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	MTAPAGRGSETERLLTPNP	GYGTQAGSPAPPTPEEDLRRRLKYFFMSPCDKFRAG	60
Db	1	MTAPAGRGSETERLLTPNP	GYGTQAGSPAPPTPEEDLRRRLKYFFMSPCDKFRAG	60
Qy	61	RKPKCLMLQVVKILVTVQLILFGLSNQLAVTFR	ENTIAFRHLFLLGYSDGADDTFAAY	120
Db	61	RKPKCLMLQVVKILVTVQLILFGLSNQLAVTFR	ENTIAFRHLFLLGYSDGADDTFAAY	120
Qy	121	TREQLYQALFHAVDQYLALPDVSLGRYAYVRGG	PWTNGSLGALCQRYHRGHVDPAND	180
Db	121	TREQLYQALFHAVDQYLALPDVSLGRYAYVRGG	PWTNGSLGALCQRYHRGHVDPAND	180
Qy	181	TFDIDPMVVTDCIQVDPPERPPPPDDTLTLESS	SSYKNLTLKFKLVNVTIHFR	LKTI 240

Db 181 TFDIDPMVVTDCIQVDPPEPPPPDDLTLLSSSSYKNLTAKFKLVNVTIHFRLKTI 240
QY 241 NLQSLINNEIPDCYTFSVLITFDNKAHSGRIPISLETQAHIECKHPSVFQHGDNFRLL 300
Db 241 NLQSLINNEIPDCYTFSVLITFDNKAHSGRIPISLETQAHIECKHPSVFQHGDNFRLL 300
QY 301 FDVVVILTCSLSFLLCARSLLRGFLQLQNEFVGFMRQRGRVISLWERLEFVNGWYILLVT 360
Db 301 FDVVVILTCSLSFLLCARSLLRGFLQLQNEFVGFMRQRGRVISLWERLEFVNGWYILLVT 360
QY 361 SDVLTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIYRLTFFHNNIILATLRV 420
Db 361 SDVLTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIYRLTFFHNNIILATLRV 420
QY 421 ALPSVMRFCCCVAVIYLGFCGWIIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFEAM 480
Db 421 ALPSVMRFCCCVAVIYLGFCGWIIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFEAM 480
QY 481 QAQGRSSLVWLFSQLYLYSFISLFYIMVLSLFIALITGAYDTIKHPGGAGAESELOAY 540
Db 481 QAQGRSSLVWLFSQLYLYSFISLFYIMVLSLFIALITGAYDTIKHPGGAGAESELOAY 540
QY 541 IAQCQDSPTSGKFRRGSGSACSLCCCGRDPSEHSLLVN 580
Db 541 IAQCQDSPTSGKFRRGSGSACSLCCCGRDPSEHSLLVN 580

RESULT 2
US-09-965-529-13
; Sequence 13, Application US/09965529
; Publication No. US20020182671A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731 USA
; CURRENT APPLICATION NUMBER: US/09/965,529
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 977658CD1
US-09-965-529-13

Query Match 100.0%; Score 3067; DB 10; Length 580;
Best Local Similarity 100.0%; Pred. No. 2.4e-289;
Matches 580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTAPAGRGSETERLLTPNPGYGTQAGSPAPPTPPEEDLRRLKYFFMSPCDKFRAG 60
Db 1 MTAPAGRGSETERLLTPNPGYGTQAGSPAPPTPPEEDLRRLKYFFMSPCDKFRAG 60
QY 61 RKPKCLMLQVVKILVVTQVQLILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAY 120
Db 61 RKPKCLMLQVVKILVVTQVQLILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAY 120
QY 121 TREQLYQAIHFAVDQYALPDVSLGRYAYVRGGDPWTNGSLALCQRYYHRGHVDPAND 180

Db 121 TREQLYQAIHFAVDQYALPDVSLGRYAYVRGGDPWTNGSLALCQRYYHRGHVDPAND 180
QY 181 TFDIDPMVVTDCIQVDPPEPPPPDDLTLLSSSSYKNLTAKFKLVNVTIHFRLKTI 240
Db 181 TFDIDPMVVTDCIQVDPPEPPPPDDLTLLSSSSYKNLTAKFKLVNVTIHFRLKTI 240
QY 241 NLQSLINNEIPDCYTFSVLITFDNKAHSGRIPISLETQAHIECKHPSVFQHGDNFRLL 300
Db 241 NLQSLINNEIPDCYTFSVLITFDNKAHSGRIPISLETQAHIECKHPSVFQHGDNFRLL 300
QY 301 FDVVVILTCSLSFLLCARSLLRGFLQLQNEFVGFMRQRGRVISLWERLEFVNGWYILLVT 360
Db 301 FDVVVILTCSLSFLLCARSLLRGFLQLQNEFVGFMRQRGRVISLWERLEFVNGWYILLVT 360
QY 361 SDVLTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIYRLTFFHNNIILATLRV 420
Db 361 SDVLTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIYRLTFFHNNIILATLRV 420
QY 421 ALPSVMRFCCCVAVIYLGFCGWIIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFEAM 480
Db 421 ALPSVMRFCCCVAVIYLGFCGWIIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFEAM 480
QY 481 QAQGRSSLVWLFSQLYLYSFISLFYIMVLSLFIALITGAYDTIKHPGGAGAESELOAY 540
Db 481 QAQGRSSLVWLFSQLYLYSFISLFYIMVLSLFIALITGAYDTIKHPGGAGAESELOAY 540
QY 541 IAQCQDSPTSGKFRRGSGSACSLCCCGRDPSEHSLLVN 580
Db 541 IAQCQDSPTSGKFRRGSGSACSLCCCGRDPSEHSLLVN 580

RESULT 3
US-09-969-680A-13
; Sequence 13, Application US/09969680A
; Publication No. US20030124649A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti; YUE, Henry
; APPLICANT: TANG, Y. Tom; BANDMAN, Olga
; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731-1 USA
; CURRENT APPLICATION NUMBER: US/09/969,680A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US00/22315
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/149,641
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/164,203
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124649A1 977658CD1
US-09-969-680A-13

Query Match 100.0%; Score 3067; DB 11; Length 580;
Best Local Similarity 100.0%; Pred. No. 2.4e-289;
Matches 580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTAPAGRGSETERLLTPNPGYGTQAGSPAPPTPPEEDLRRLKYFFMSPCDKFRAG 60
Db 1 MTAPAGRGSETERLLTPNPGYGTQAGSPAPPTPPEEDLRRLKYFFMSPCDKFRAG 60
QY 61 RKPKCLMLQVVKILVVTQVQLILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAY 120
Db 61 RKPKCLMLQVVKILVVTQVQLILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAY 120

QY 121 TREQLYQAIHFAVDQYLALPDVSLGRYAYVRGGDPWTNGSLALCQRYHHRGHVDPAND 180
Db 121 TREQLYQAIHFAVDQYLALPDVSLGRYAYVRGGDPWTNGSLALCQRYHHRGHVDPAND 180
QY 181 TFDIDPMVVTDCIQVDPPEPPPPDDDLTLLSSSSYKNLTCLKFKLVNVTIHFRLKTI 240
Db 181 TFDIDPMVVTDCIQVDPPEPPPPDDDLTLLSSSSYKNLTCLKFKLVNVTIHFRLKTI 240
QY 241 NLQSLINNEIPDCYTFSVLITFDNKAHSGRIPISLETQAHIQECKHPSVFQHGDNFSRLL 300
Db 241 NLQSLINNEIPDCYTFSVLITFDNKAHSGRIPISLETQAHIQECKHPSVFQHGDNFSRLL 300
QY 301 FDVVVILTCSLFLLCARSLLRGFLLLQNEFVGFMMWRQGRVISLWERLEFVNGWYILLVT 360
Db 301 FDVVVILTCSLFLLCARSLLRGFLLLQNEFVGFMMWRQGRVISLWERLEFVNGWYILLVT 360
QY 361 SDVLTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIIRYLTFFHNYNILIATLRV 420
Db 361 SDVLTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIIRYLTFFHNYNILIATLRV 420
QY 421 ALPSVMRFCCCVAVIYLGCFCGWIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFEAM 480
Db 421 ALPSVMRFCCCVAVIYLGCFCGWIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFEAM 480
QY 481 QAQQGRSSLVWLFSQLYLYSFISLFYIMVLSLFIALITGAYDTIKHPGGAGAESELOAY 540
Db 481 QAQQGRSSLVWLFSQLYLYSFISLFYIMVLSLFIALITGAYDTIKHPGGAGAESELOAY 540
QY 541 IAQCQDSPTSGKFRRGSGSACSLCCCGRDPSEHSLLVN 580
Db 541 IAQCQDSPTSGKFRRGSGSACSLCCCGRDPSEHSLLVN 580

RESULT 4

US-10-103-458-2
; Sequence 2, Application US/10103458
; Publication No. US20020197680A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
; FILE REFERENCE: MNI-125
; CURRENT APPLICATION NUMBER: US/10/103,458
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US/09/544,797
; PRIOR FILING DATE: PEIOE FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-103-458-2

Query Match 100.0%; Score 3067; DB 14; Length 580;
Best Local Similarity 100.0%; Pred. No. 2.4e-289;
Matches 580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTAPAGPRGSETERLLTPNPGYGTQAGSPAPPTPPEEEDLRRLKYFFMSPCDKFRAG 60
Db 1 MTAPAGPRGSETERLLTPNPGYGTQAGSPAPPTPPEEEDLRRLKYFFMSPCDKFRAG 60
QY 61 RKPKCLMLQVVKILVVTQVLIILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAY 120
Db 61 RKPKCLMLQVVKILVVTQVLIILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAY 120
QY 121 TREQLYQAIHFAVDQYLALPDVSLGRYAYVRGGDPWTNGSLALCQRYHHRGHVDPAND 180
Db 121 TREQLYQAIHFAVDQYLALPDVSLGRYAYVRGGDPWTNGSLALCQRYHHRGHVDPAND 180
QY 181 TFDIDPMVVTDCIQVDPPEPPPPDDDLTLLSSSSYKNLTCLKFKLVNVTIHFRLKTI 240
Db 181 TFDIDPMVVTDCIQVDPPEPPPPDDDLTLLSSSSYKNLTCLKFKLVNVTIHFRLKTI 240

QY 241 NLQSLINNEIPDCYTFSVLITFDNKAHSGRIPISLETQAHIQECKHPSVFQHGDNFSRLL 300
Db 241 NLQSLINNEIPDCYTFSVLITFDNKAHSGRIPISLETQAHIQECKHPSVFQHGDNFSRLL 300
QY 301 FDVVVILTCSLFLLCARSLLRGFLLLQNEFVGFMMWRQGRVISLWERLEFVNGWYILLVT 360
Db 301 FDVVVILTCSLFLLCARSLLRGFLLLQNEFVGFMMWRQGRVISLWERLEFVNGWYILLVT 360
QY 361 SDVLTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIIRYLTFFHNYNILIATLRV 420
Db 361 SDVLTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIIRYLTFFHNYNILIATLRV 420
QY 421 ALPSVMRFCCCVAVIYLGCFCGWIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFEAM 480
Db 421 ALPSVMRFCCCVAVIYLGCFCGWIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFEAM 480
QY 481 QAQQGRSSLVWLFSQLYLYSFISLFYIMVLSLFIALITGAYDTIKHPGGAGAESELOAY 540
Db 481 QAQQGRSSLVWLFSQLYLYSFISLFYIMVLSLFIALITGAYDTIKHPGGAGAESELOAY 540
QY 541 IAQCQDSPTSGKFRRGSGSACSLCCCGRDPSEHSLLVN 580
Db 541 IAQCQDSPTSGKFRRGSGSACSLCCCGRDPSEHSLLVN 580

RESULT 5

US-09-820-893-63
; Sequence 63, Application US/09820893
; Patent No. US20020076705A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 31 Human Secreted Proteins
; FILE REFERENCE: PZ033PI
; CURRENT APPLICATION NUMBER: US/09/820,893
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/531,119
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/102,895
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (135)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-820-893-63

Query Match 86.9%; Score 2665; DB 9; Length 511;
Best Local Similarity 99.2%; Pred. No. 2.5e-250;
Matches 507; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 70 VVKILVVTQVLIILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAYTREQLYQAI 129
Db 1 VVKILVVTQVLIILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAYTREQLYQAI 60
QY 130 FHAVDQYLALPDVSLGRYAYVRGGDPWTNGSLALCQRYHHRGHVDPANDTDFIDPMV 189
Db 61 FHAVDQYLALPDVSLGRYAYVRGGDPWTNGSLALCQRYHHRGHVDPANDTDFIDPMV 120
QY 190 TDCIQVDPPEPPPPDDDLTLLSSSSYKNLTCLKFKLVNVTIHFRLKTIINQSLINNE 249
Db 121 TDCIQVDPPEPPPPDDDLTLLSSSSYKNLTCLKFKLVNVTIHFRLKTIINQSLINNE 180
QY 250 IPDCYTFSVLITFDNKAHSGRIPISLETQAHIQECKHPSVFQHGDNFSRLLFDVVVILTC 309
Db 181 IPDCYTFSVLITFDNKAHSGRIPISLETQAHIQECKHPSVFQHGDNFSRLLFDVVVILTC 240
QY 310 SLSFLLCARSLLRGFLLLQNEFVGFMMWRQGRVISLWERLEFVNGWYILLVTSVLTISGT 369


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Db 241 SLSFLLCARSLRGFLLLQNEFVGFMWRQGRVISLWERLEFVNGWYILLVTSVLTISGT 300
QY 370 IMKIGIEAKNLASYDVCSILLGTSTLLVWGVIRYLTFFHNNILIAITLRVALPSVMRFC 429
Db 301 IMKIGIEAKNLASYDVCSILLGTSTLLVWGVIRYLTFFHNNILIAITLRVALPSVMRFC 360
QY 430 CCVAVIYLGFCGWIIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFAMQAQQGRSSL 489
Db 361 CCVAVIYLGFCGWIIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFAMQAQQGRSSL 420
QY 490 VWLFSQLYLSFISLFYIMVLSLFIALITGAYDTIKHPGGAGAESELOAYIAQCQDSPT 549
Db 421 VWLFSQLYLSFISLFYIMVLSLFIALITGAYDTIKHPGGAGAESELOAYIAQCQDSPT 480
QY 550 SGKFRGGSGSACSLCCCGRDPSEHSLLVN 580
Db 481 SGKFRGGSGSACSLCCCGRDPSEHSLLVN 511

RESULT 6
US-10-114-153-26
; Sequence 26, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennnda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACID SEQUENCES, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; PRIOR FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
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; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 26
; LENGTH: 538
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-114-153-26

Query Match 44.9%; Score 1376; DB 12; Length 538;
Best Local Similarity 48.9%; Pred. No. 7.1e-125;
Matches 268; Conservative 115; Mismatches 143; Indels 22; Gaps 8;

QY 37 EEEDLRRRLKYFFMSPCDKFRKGRKPKMLQVVKILVTVQLILFGLSNOLAVTFREE 96
Db 9 KEECLREDLKFFMSPCEKYRARRQIPWKLGLQILKIVMVTTLQVRFGLSNQLVAFKED 68
QY 97 NTIAFRHLFLGYSDGADDTF--AAYTREQLYQAFHVAVDQYLALPDVSLGRYAYVRGGG 154
Db 69 NTVAFKHLFLKGYSGTDEDDYSCSVYTOEDAYESIFFAINQYHQLKDIITLGLGY---G 124
QY 155 DPWTNGSGLALCQRYHHRGHVDPANDTFDIDMVVTDCTIQVDPPPPPPDDLTLLS 214
Db 125 ENEDNRIGLVCKQHYKGTMTFSPNETLINDVELDCVQLDLQDLKPPD-----WKN 179
QY 215 SSSYKNLTLLKFKHLVNVITHFRKLTINLQSLINNEIPDCYTFSVLITFDNKAHSGRIPIS 274
Db 180 SSFPR---LEFYRLQLQVEISFHLKGIDLQTIHSRELPCYVFQNTIIFDNKAHSGKIKY 236
QY 275 LETQAHIQECKHPSVFOHGDNS--FRLLFDVVVILTCSLFLLCARSLRGLLQNEFVG 332
Db 237 FDSDAKIEECKDLNIFGSAQKNAQYVLVDFDAFVIVICLASLILCTRSIVLALRLKRFN 296
QY 333 FMWRQGRVISLWERLEFVNGWYILLVTSVLTISGTIMKIGIEAKNLASYDVCSILLGT 392
Db 297 FFLEKYKRPVCDTDQWEFINGWYLVIIISDLMTIIGSILKMEIKAKNLTYDLCSIFLGT 356
QY 393 STILLVWVGVIYRLTFFHNNILIAITLRVALPSVMRECCCVAVIYLGFCGWIIVLGPYHV 452
Db 357 STILLVWVGVIYRLGYFQAYNVILITMQASLPKVLRFACAGMIYLGTYFCGWIIVLGPYHD 416
QY 453 KFRSLSMVSECLFSLINGDDMFVTFAMQAQQGRSSLVWLPFSQLYLSFISLFYIMVLSL 512
Db 417 KFEENLTVAECLFSLVNGDDMFATFA--QIQQ-KSILVWLFSLYLSFISLFYIMVLSL 473
QY 513 FIALITGAYDTIKHPGGAGAESELOAYIAQCQDSPTSGKFRGGSGSACSLCCCGRDP 572
Db 474 FIALITDSYDTIKKFGQNGFPETDLQEFLEKCS--SKEEYQKESAFSLSCICRRRKRS 530
QY 573 BEHSLLVN 580
Db 531 DDHLIPIS 538
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```
RESULT 7
US-10-114-153-28
; Sequence 28, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennnda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
```

```
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC AC
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 28
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-153-28

Query Match 44.6%; Score 1368; DB 12; Length 566;
Best Local Similarity 48.7%; Pred. No. 4.6e-124;
Matches 267; Conservative 115; Mismatches 144; Indels 22; Gaps 8;

QY 37 EEEDLRRRLKYFPWSPCDKFRAGKRPCKIMLQVVKILVTVVQLILFGLSNQLAVTFREE 96
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 37 KEECLREDLKFCYCMSPCEKYRARRQIPWKLGLQILKIVMTQVLRFGLSNQLVAVKED 96
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 97 NTIAFRHLFLGLYSDGADDTF--AAYTREQLYQAIHFAVDQYLALPDVSLGRVAYVRGGG 154
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 97 NTVAFKHLFLKGYSGTDEDDYSVYQEDAYESIFFAINGYHQLKIDITLGLGY----G 152
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 155 DPWTNGSGLALCQRYHRGHVDPANDTFIDPMVVTDCIQVDPPEPPPPPSDDLTLLES 214
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 153 ENEDNRIGLVKVCQHYKKGTMFSPNETLNDNDVELDCVQLDLQDLSKKPPD-----WKN 207
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 215 SSSYKNLTLKFKHLVNVTHIFRLKTNLQSLINNEIPDCYTFSVLITFDNKAHSGRIPIS 274
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 208 SSFFR---LEFYRLQLVEISFHLKGIDLQTIHSRELPCYVFQNTIIFDNKAHSGKIKIY 264
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 275 LETQAHIQECKHPSVQFHGDNS--FRLLFDVWVILTCSLSLCARSLLRGFLIQNEFVG 332
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
Db 265 FDSDAKIECKDLNIFGSAQKNAQYVLVDFDAFVIVICLASLILCTRSIVLALRLKRFNL 324
QY 333 FMWRQGRVIVSLWERLEFVNGWYILLVTSDVLTISGTIMKIGIEAKNLASYDVCSILLGT 392
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 325 FFLEKYKRPVCDTDQWEFINGWYVLVVIISDLMTIIGSILKMEIKAKNLTYDLCSIFLGT 384
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 393 STLLVWVGVIIRYLTFFHNYNLIATLRVALPSVNRFFCCCVAVIYLGKFCGWIIVLGPYHV 452
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 385 STLLVWVGVIIRYLYGYFQAYNVLIITMQASLPKVLRFCAACAGMIYLYGTFCGWIVLGPYHD 444
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 453 KFRSLSMVSECLFSLINGDDMFVTFAMQAQQGSSSLVWLFSQLYLYSFLIYMWLSL 512
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 445 KFENLNTVAECLFSLVNGDDMFATFA--QIQQ-KSILVWLFESRLYLYSFLIYMWLSL 501
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 513 FIALITGAYDTIKHPGGAGAESESELQAYIAQCQDSPTSGKFRRGSGSACSLCCCGRDPS 572
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 502 FIALITDSYDTIKKFOQNGFPETDLQEFLEKES---SKEEYQKESAFLESCICRRRKR 558
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 573 EEHSLLVN 580
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 559 DDHLIPIS 566

RESULT 8
US-10-114-153-24
; Sequence 24, Application US/10/114153
; Publication No. US20030185815A1.
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekkuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC AC
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
```

```
Matches 124; Conservative 31; Mismatches 31; Indels 0; Gaps 0;
QY 299 LLFDVVVILTCSLFLLCARSLRGFLQLONEFVGFWMRQGRVISLWERLEFVNGWYILL 358
Db 2 MIFDAFVILTCVLSLILCIRSIVIRGLQLQEQEFVNFLLHYKKEVSVDQMEFVNGWYIMI 61
QY 359 VTSVDVLTISGTMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIYRLTFFHNNIATL 418
Db 62 IISDILTIIIGSILKMEIQAKSLTSYDVCSILLGTSTMLVWLVGVIYRLGFAKYNLLILT 121
QY 419 RVALPSVMRFCCCVAVIYLGFCFCGWIIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTF 478
Db 122 QAALPNVIRFCCCAAMIYLGFCFCGWIIVLGPYHDKFRSLNMVSECLFSLINGDDMFATFA 181
QY 479 AMQAQQ 484
Db 182 KMQKK 187

RESULT 12
US-09-864-761-45089
; Sequence 45089, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45089
; LENGTH: 69
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC013291.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.57
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.46
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.46
; OTHER INFORMATION: EST HUMAN HIT: N41861.1, EVALUE 5.00e-28
; OTHER INFORMATION: SWISSPROT HIT: Q13563, EVALUE 7.00e-03
US-09-864-761-45089
Query Match 9.2%; Score 281.5; DB 9; Length 69;
Best Local Similarity 79.2%; Pred. No. 1.1e-19;
Matches 57; Conservative 6; Mismatches 6; Indels 3; Gaps 1;
QY 454 FRSLSMVSECLFSLINGDDMFVTFPAAMQAQQGRSSLVWLFSQLYLSFISLFIYMWLSLF 513
Db 1 FRSLNMVSECLFSLINGDDMFATFAKMQQ---KSYLVWLFSLRIYLSFISLFIYMWLSLF 57
QY 514 IALITGAYDTIK 525
Db 58 IALITDTYETIK 69

RESULT 13
US-10-005-211-2
; Sequence 2, Application US/10005211
; Publication No. US20020194636A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING
; TITLE OF INVENTION: POLYCYSTIN-RELATED GENE DISRUPTIONS
; FILE REFERENCE: R-325
; CURRENT APPLICATION NUMBER: US/10/005,211
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/256,201
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 60/250,999
; PRIOR FILING DATE: 2000-12-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-005-211-2
Query Match 5.0%; Score 152.5; DB 14; Length 621;
Best Local Similarity 21.5%; Pred. No. 9.6e-06;
Matches 52; Conservative 45; Mismatches 98; Indels 47; Gaps 8;
QY 306 ILTCSLSFLLCARSLLRGFLLLQ-----NEFVGFMWRQGRVISLWERLEFVNGWYILLVT 360
Db 282 IASCEVIFCI---FLFVFIQELRKVNEFKSAYFR-----SVWNWLE-----MLLLL 325
QY 361 SDVLTIS-----GTMKIGIEAKNLASYDVCSIL-----LGTSTLLVWVGVI 403
Db 326 LCFLAVSFYAYCNMQSFLLGQLLKNTDSYPDFLAYWHIYNNVIAITIFFAWIKIFK 385
QY 404 YLTFPHNNIATLRVALPSVMRFCCCVAVIYLGFCFCGWIIVLGPYHVKFRSLSMVSEC 463
Db 386 FISFNETMSQLSLSRCKMDIVGFAIMFFIIPSAYAQLGFLVFGSQVDDPFSTFQNSIFA 445
QY 464 LFSLINGDDMFVTFPAAMQAQQGRSSLVWLFSQLYLSFISLFIYMWLSLFIALITGAYDT 523
Db 446 QFRIVLGD---FNFAGIQQAN-----WILGPIYFITIFFVFFVLLNMFALINDTYSE 496
QY 524 IK 525
Db 497 VK 498

RESULT 14
```

```
US-09-828-466-6
; Sequence 6, Application US/09828466
; Patent No. US20020035056A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
; FILE REFERENCE: MNI-125CP
; CURRENT APPLICATION NUMBER: US/09/828,466
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/544,797
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 6
; LENGTH: 966
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-466-6

Query Match      5.0%; Score 152.5; DB 9; Length 966;
Best Local Similarity 21.3%; Pred. No. 1.8e-05;
Matches 59; Conservative 49; Mismatches 104; Indels 65; Gaps 10;

QY      296 SFRLFDVVVILTCSLSFLL-----CARSLRGFLQLQNEFVGEMWRQGRVISLWERLE 349
Db      503 SFWNCLDVIVVLSVVAMVINIYRMSNAEGLLQFLEDQNSFPNF-----E 547

QY      350 FVNGWYILLVTSVLTISGTIMKIGIEAKNLSYDVCSILLGTSTLLVWVGIVIRYLTPFH 409
Db      548 HVAYWQ-----IQFNNISAVMV-----FLVWIKLKFKNFNR 579

QY      410 NYNILIAIATRLVALPSVMRFCCVAVIYLGVCYCGWIVLGPYHVKFRSLSMVSECLFS--- 466
Db      580 TMSQLSTTMSRCAKDLFGFTIMFSIIFLAYAQLAYLVFG---TQVDDFSTFOECIFQPR 636

QY      467 LINGDDMFVTFAAMQAQQGRSSLVWLFSQLYLYSFISLFYIMVLSLFIALITGAYDTIKH 526
Db      637 IILGD---INFAEIB-EANR-----VLGPLYFTTFVFFMFFILLNMFLAIINDSYSEVKS 687

QY      527 PGGAGAESELSQAYIAQ-CQDSPTSGKFRGSGSACS 562
Db      688 SVAQQAEMELSDLRKGCQKALVKLKLKRNVTVDAIS 724

RESULT 15
US-09-864-761-41295
; Sequence 41295, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 41295
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC013291.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
; OTHER INFORMATION: EST_HUMAN HIT: BF111413.1, EVALUUE 1.00e-30
US-09-864-761-41295

Query Match      4.9%; Score 150.5; DB 9; Length 76;
Best Local Similarity 54.9%; Pred. No. 7e-07;
Matches 28; Conservative 11; Mismatches 7; Indels 5; Gaps 1;

QY      34 TPPEEE-----DLRRRLKYFFMSPCDKFRAGKGRKPKMLQVVKILVVTVQ 79
Db      26 TSPSEELLLEDDQMRRLKLFKFFFMNPFCEKFWARGKRPWKLAIQILKIAMVTIQ 76
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Search completed: October 27, 2003, 18:15:32
Job time : 446 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

QM protein - protein search, using sw model

Run on: October 27, 2003, 17:43:58 ; Search time 90 Seconds
(without alignments)
1663.006 Million cell updates/sec

Title: US-09-851-494B-3
Perfect score: 3067
Sequence: 1 MTAPAGPRGSETERLLTPNP.....CSLLCCCGRDPSEHSLVN 580

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 23:*

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvivirus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3067	100.0	580	4 Q9GZU1	Q9gzul homo sapien
2	3059	99.7	580	4 Q9H4B3	Q9h4b3 homo sapien
3	2884.5	94.0	581	4 Q9H292	Q9h292 homo sapien
4	2820	91.9	580	11 Q99J21	Q99j21 mus musculu
5	1859.5	60.6	545	4 Q9H4B5	Q9h4b5 homo sapien
6	1628.5	53.1	594	11 Q8BS73	Q8bs73 mus musculu
7	1626.5	53.0	553	11 Q8R4F0	Q8r4f0 mus musculu
8	1626.5	53.0	591	11 Q8BSG1	Q8bsg1 mus musculu
9	1623.5	52.9	593	11 Q8CDB2	Q8cdb2 mus musculu
10	1621	52.9	553	4 Q8TDD5	Q8td5 homo sapien
11	1396	45.5	497	4 Q9NV09	Q9nv09 homo sapien
12	1374	44.8	538	4 Q8IZK6	Q8izk6 homo sapien
13	1335	43.5	538	11 Q9CQD3	Q9cq3 mus musculu
14	1335	43.5	566	11 Q8K595	Q8k595 mus musculu
15	1332	43.4	538	11 Q8K2T6	Q8k2t6 mus musculu
16	1025.5	33.4	652	5 Q9VW35	Q9vw35 drosophila

17	783	25.5	609	5	Q8T877	Q8t877 caenorhabdi
18	783	25.5	666	5	Q8T878	Q8t878 caenorhabdi
19	777	25.3	611	5	Q9BJ56	Q9bj56 caenorhabdi
20	777	25.3	668	5	Q8T666	Q8t666 caenorhabdi
21	776	25.3	644	5	Q8WSP3	Q8wsp3 caenorhabdi
22	385	12.6	175	4	Q8N9R3	Q8n9r3 homo sapien
23	161.5	5.3	897	5	Q9VK95	Q9vk95 drosophila
24	151.5	4.9	966	11	Q8BPR6	Q8bpr6 mus musculu
25	139.5	4.5	660	13	Q8AW53	Q8aw53 brachydanio
26	127.5	4.2	199	11	Q8C0Z9	Q8c0z9 mus musculu
27	125	4.1	733	10	Q948T1	Q948t1 arabidopsis
28	124	4.0	665	4	Q95814	Q95814 homo sapien
29	123	4.0	724	10	Q9ZT83	Q9zt83 arabidopsis
30	123	4.0	733	10	Q94KI8	Q94ki8 arabidopsis
31	115.5	3.8	1274	5	Q9V5Q9	Q9vsq9 drosophila
32	115	3.7	420	8	Q8HN35	Q8hn35 paragonimus
33	115	3.7	482	12	Q81013	Q81013 herpesvirus
34	111.5	3.6	775	5	Q9UI57	Q9uis7 caenorhabdi
35	111.5	3.6	2300	5	Q8IP23	Q8ip23 drosophila
36	111.5	3.6	2516	5	Q9V3P7	Q9v3p7 drosophila
37	111.5	3.6	2519	5	Q8IP25	Q8ip25 drosophila
38	111.5	3.6	2552	5	Q8IP24	Q8ip24 drosophila
39	111	3.6	321	16	Q8CNG5	Q8cng5 staphylococ
40	111	3.6	400	16	Q97ER0	Q97er0 clostridium
41	110.5	3.6	310	8	P92079	P92079 menosoma ci
42	109	3.6	420	8	Q9MLH8	Q9mlh8 paragonimus
43	109	3.6	793	3	Q08967	Q08967 saccharomyc
44	108.5	3.5	2196	5	P91744	P91744 loligo blee
45	108	3.5	2221	5	Q9NKV1	Q9nkv1 halocynthia

ALIGNMENTS

RESULT 1

Q9GZU1	PRELIMINARY;	PRT;	580 AA.
AC Q9GZU1;			
DT 01-MAR-2001 (Tremblrel. 16, Created)			
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)			
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)			
DE Hypothetical protein FLJ22449 (Mucolipin) (Mucolipidosis type IV protein) (Mucolipin 1).			
GN MCOLN1 OR MLIV.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,			
RA Okitani R., Ota T., Suzuki Y., Ohayashi M., Nishi T., Shibahara T.,			
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;			
RT "NEDO human cDNA sequencing project.";			
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.			
RN [2]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=20485419; PubMed=11030752;			
RA Sun M., Goldin E., Stahl S., Falardeau J.L., Kennedy J.C.,			
RA Acierno J.S. Jr., Bove C., Kaneski C.R., Nagle J., Bromley M.C.,			
RA Colman M., Schiffmann R., Slaughter S.A.;			
RT "Mucopolidosis type IV is caused by mutations in a gene encoding a novel transient receptor potential channel.";			
RL Hum. Mol. Genet. 9:2471-2478(2000).			
RN [3]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=20428196; PubMed=10973263;			
RA Bargal R., Avidan N., Ben-Asher E., Olender Z., Zeigler M.,			
RA Frumkin A., Raas-Rothschild A., Glusman G., Lancet D., Bach G.;			
RT "Identification of the gene causing mucopolidosis type IV.";			
RL Nat. Genet. 26:118-121(2000).			
RN [4]			
RP SEQUENCE FROM N.A.			

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20428196; PubMed=10973263;
RA Bargal R., Avidan N., Ben-Asher E., Olender Z., Zeigler M.,
RA Frumkin A., Raas-Rothschild A., Glusman G., Lancet D., Bach G.;
RT "Identification of the gene causing mucopolipidosis type IV";
RL Nat. Genet. 26:118-123(2000).
DR EMBL; AF305579; AAG42242.1; -
DR EMBL; AF305572; AAG42242.1; JOINED.
DR EMBL; AF305573; AAG42242.1; JOINED.
DR EMBL; AF305574; AAG42242.1; JOINED.
DR EMBL; AF305575; AAG42242.1; JOINED.
DR EMBL; AF305576; AAG42242.1; JOINED.
DR EMBL; AF305577; AAG42242.1; JOINED.
DR EMBL; AF305578; AAG42242.1; JOINED.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000734; Lipase.
DR Pfam; PF00520; ion_trans; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 581 AA; 65099 MW; 342B4B558C891112 CRC64;

Query Match 94.0%; Score 2884.5; DB 4; Length 581;
Best Local Similarity 94.9%; Pred. No. 1.1e-248;
Matches 555; Conservative 5; Mismatches 16; Indels 9; Gaps 2;
QY 1 MTAPAGPRGSETERLLTPNPGYGTQAGSPAPPTPEEEDLRRRLKYFFMSPCDKFRAG 60
Db 1 MTAPAGPRGSETERLLTPNPGYGTQAGSPAPPTPEEEDLRRRLKYFFMSPCDKFRAG 60
QY 61 RKPKKLMQVVKILVVTQVQLILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAY 120
Db 61 RKPKKLMQVVKILVVTQVQLILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAY 120
QY 121 TREQLYQAIHFAVDQYLALPDVSLGRYAYVRGGDPWTNGSL-----ALCQRYHGRHV 175
Db 121 TREQLYQAIHFAVDQYLALPDVSLGRYAYVRGGDPWTNGSL--SASGTTTEATWTR-- 177
QY 176 DPANDTFDIDPMVVTDCIQVDPPEPPPPSDDTLTLESSSYKNLTALKFKLVNVTIHF 235
Db 178 -PTTHLTLRWLLVNCIQVDPPEPPPPSDDTLTLESSSYKNLTALKFKLVNVTIHF 236
QY 236 RLKTLNQLINNEIPDCYTFSVLITFDNKAHSGRIPISLETQAHIECKHPSVFQHGDN 295
Db 237 RLKTLNQLINNEIPDCYTFSVLITFDNKAHSGRIPISLETQAHIECKHPSVFQHGDN 296
QY 296 SFRLLFVTVVLTCSLSFLLCARSLLRGLLQNEFVGFWMRQGRVISLWERLEFVNGWY 355
Db 297 SFRLLFVTVVLTCSLSFLLCARSLLRGLLQNEFVGFWMRQGRVISLWERLEFVNGWY 356
QY 356 ILLVTSVLTISGTMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIIRYLTFFHNNILI 415
Db 357 ILLVTSVLTISGTMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIIRYLTFFHNNILI 416
QY 416 ATRLVALPSVMRFFCCCVAVIYLGFCGWIIVLGPYHVKFRSLSMVSECLFSLINGDDMFV 475
Db 417 ATRLVALPSVMRFFCCCVAVIYLGFCGWIIVLGPYHVKFRSLSMVSECLFSLINGDDMFV 476
QY 476 TFAAMQAQGRSSLVWLFSQLYLSFISLFYIMVLSLFIALTITGAYDTIKHPGGAGABES 535
Db 477 TFAAMQAQGRSSLVWLFSQLYLSFISLFYIMVLSLFIALTITGAYDTIKHPGGAGABES 536
QY 536 ELQAYIAQCDSPTSGKFRRGSGSACSLCCCGRDPSEHSLVN 580
Db 537 ELQAYIAQCDSPTSGKFRRGSGSACSLCCCGRDPSEHSLVN 581

Q99J21
ID Q99J21 PRELIMINARY; PRT; 580 AA.
AC Q99J21;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Mucolipin-1.
GN MCOLN1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Falardeau J.L., Kennedy J.C., Acierno J.S., Sun M., Stahl S.,
RA Goldin E., Slangenaupt S.A.;
RT "Cloning and characterization of the mouse Mcoln1 gene.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Diencephalon, Extraembryonic tissue, Placenta, and Spinal cord;
RX MEDLINE=22354583; PubMed=12466851;
RA The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).";
DR EMBL; BC005651; AAH05651.1; -
DR EMBL; AF302009; AAL58667.1; -
DR EMBL; AK028385; BAC25922.1; -
DR EMBL; AK034471; BAC28719.1; -
DR EMBL; AK049606; BAC33838.1; -
DR MGD; MGI:1890498; Mcoln1.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000734; Lipase.
DR Pfam; PF00520; ion_trans; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 580 AA; 65505 MW; F64D2E6C5D4C041C CRC64;
Query Match 91.9%; Score 2820; DB 11; Length 580;
Best Local Similarity 91.4%; Pred. No. 6.5e-243;
Matches 530; Conservative 18; Mismatches 32; Indels 0; Gaps 0;
QY 1 MTAPAGPRGSETERLLTPNPGYGTQAGSPAPPTPEEEDLRRRLKYFFMSPCDKFRAG 60
Db 1 MATPAGRRASETERLLTPNPGYGTQVGTSPAPPTPEEEDLRRRLKYFFMSPCDKFRAG 60
QY 61 RKPKKLMQVVKILVVTQVQLILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAY 120
Db 61 RKPKKLMQVVKILVVTQVQLILFGLSNQLAVTFREENTIAFRHLFLLGYSDGADDTFAAY 120
QY 121 TREQLYQAIHFAVDQYLALPDVSLGRYAYVRGGDPWTNGSLALCQRYHGRHVDPAND 180
Db 121 TQEQLYQAIIFYAVDQYLILPEISLGRYAYVRGGGPGWANGSALALCQRYHGRHVDPAND 180
QY 181 TFDIDPMVVTDCIQVDPPEPPPPSDDTLTLESSSYKNLTALKFKLVNVTIHFRLKTI 240
Db 181 TFDIDPRVVTDCIQVDPPEPPPPDIPSEDLDFLDGSASYKNLTALKFKLVNVTIHFQLKTI 240
QY 241 NLOSLINNEIPDCYTFSVLITFDNKAHSGRIPISLETQAHIECKHPSVFQHGDNFRL 300
Db 241 NLOSLINNEIPDCYTFSVLITFDNKAHSGRIPISLETQAHIECKHPSVSRHGDNFRL 300
QY 301 FDVVVILTCSLSFLLCARSLLRGLLQNEFVGFWMRQGRVISLWERLEFVNGWYILLVT 360

Db 301 FDVVVILCSLSFLLCARSLRGLLQNEFVFWFMRRRGRISLWERLEFVNGWILLVT 360

QY 361 SDVLTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGIRYLTFFHNYNILLATLRV 420

Db 361 SDVLTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGIRYLTFFHNYNILLATLRV 420

QY 421 ALPSVMRFCCCVAVIYLYGCFCGWIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFAM 480

Db 421 ALPSVMRFCCCVAVIYLYGCFCGWIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFAM 480

QY 481 QAQQRSSLVWLFSQLYLYSFISFIYMWLSLFIALITGAYDTIKHPGGAGAESELOAY 540

Db 481 QAQQGHSSLVWLFSQLYLYSFISFIYMWLSLFIALITGAYDTIKHPGGGTGTEKSELQAY 540

QY 541 IAQCQDSPTSGKFRRGSGSACSLCCCGRDPSEHSLVN 580

Db 541 IEQCQDSPTSGKFRRGSGSACSLFCCCGRDSPEHSLVN 580

RESULT 5

Q9H4B5 PRELIMINARY; PRT; 545 AA.

ID Q9H4B5

AC Q9H4B5

DT 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)

DE Mucolipidin.

GN ML4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Bassi M.T., Manzoni M., Monti E., Pizzo M.T., Ballabio A., Borsani G.;

RT "Cloning of the gene encoding a novel integral membrane protein, mucleipidin, and identification of the two major founder mutations causing mucleipidosis type IV";

RL Am. J. Hum. Genet. 67:1110-1120 (2000).

DR EMBL; AJ293659; CAC07813.1; -

DR InterPro; IPR002111; Cat_channel_TrpL.

DR InterPro; IPR005821; Ion_trans.

DR Pfam; PF00520; ion_trans; 1.

KW Ionic channel; Transmembrane.

SQ SEQUENCE 545 AA; 60608 MW; 55179F72029D65C3 CRC64;

Query Match 60.6%; Score 1859.5; DB 4; Length 545;

Best Local Similarity 93.8%; Pred. No. 3e-157;

Matches 360; Conservative 2; Mismatches 5; Indels 17; Gaps 2;

QY 197 PPERPPPPSDDLTLLESSSSYKNTLKFHKLNVNTHFRLKTINLQSLINNEIPDCYTF 256

Db 179 PEDAPDPHPS-----LLP-----RLNVNTHFRLKTINLQSLINNEIPDCYTF 221

QY 257 SVLITFDNKAHSGRIPISLETQAHIOECKHPSVFQHGDNFRLFDVVVILTCSLSFLLC 316

Db 222 SVLITFDNKAHSGRIPISLETQAHIOECKHPSVFQHGDNFRLFDVVVILTCSLSFLLC 281

QY 317 ARSLRGLLQNEFVGFWMRQRGRVISLWERLEFVNGWYILLVTSVLTISGTIMKIGIE 376

Db 282 ARSLRGLLQNEFVGFWMRQRGRVISLWERLEFVNGWYILLVTSVLTISGTIMKIGIE 341

QY 377 AKNLASYDVCSILLGTSTLLVWVGIRYLTFFHNYNILLATLRVALPSVMRFCCCVAVIY 436

Db 342 AKNLASYDVCSILLGTSTLLVWVGIRYLTFFHNYNILLATLRVALPSVMRFCCCVAVIY 401

QY 437 LGYCFCGWIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFAMQAQQRSSLVWLFSQL 496

Db 402 LGYCFCGWIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFAMQAQQRSSLVWLFSQL 461

QY 497 YLYSFISLFIYMWLSLFIALITGAYDTIKHPGGAGAESELOAYIAQCQDSPTSGKFRRG 556

Db 462 YLYSFISLFIYMWLSLFIALITGAYDTIKHPGGAGAESELOAYIAQCQDSPTSGKFRRG 521

QY 557 SGSACSLCCCGRDPSEHSLVN 580

Db 522 SGSACSLCCCGRDPSEHSLVN 545

RESULT 6

Q8BS73 PRELIMINARY; PRT; 594 AA.

ID Q8BS73

AC Q8BS73

DT 01-MAR-2003 (Tremblrel. 23, Created)

DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)

DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)

DE Weakly similar to MUCOLIPIDIN (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";

RL Nature 420:563-573 (2002).

DR EMBL; AK035029; BAC28916.1; -

FT NON TER 1

SQ SEQUENCE 594 AA; 68259 MW; 958DA443C786E45C CRC64;

Query Match 53.1%; Score 1628.5; DB 11; Length 594;

Best Local Similarity 55.5%; Pred. No. 1.4e-136;

Matches 313; Conservative 91; Mismatches 121; Indels 39; Gaps 6;

QY 7 PRGSETERLLTPNPGYGTQAGSPAPPTPEEEDLRRRLKYFFMSPCDKFRAGKRPCKL 66

Db 65 PSSSPSEQLLL-----EDQMRRLKLFNPNPCEKFWARGKPKWL 104

QY 67 MLQVVKILVTVQILFLGLSNQLAVTFRRENTIAFRHLFLGLGSDGADDTFAAYTREQLY 126

Db 105 AIQILKIAMVTIQLVFLGLSNQMVVAFKENTIAFKHLFLKGYMDRMDDTYAVYTQSEVY 164

QY 127 QAIFHAVDQYLALPDVSLGRYAYVRGGDPWTNGSLALCORYHRGHVDPANDTFDIDP 186

Db 165 DOIIFAVTQYLQNLQNISVGNHAYENKG---TKQSAMAICQHPYRQGTICPGNDTFDIDP 220

QY 187 MVVTDCIQVDPPERPPPPSDDLTLLESSSSYK-NLTLKFHKLNVNTHFRLKTINLQSL 245

Db 221 EVETECFLVEP-----DEASHLGTGPKGNLNLSDLFHRLTLVELQFKLKAINLQTV 271

QY 246 INNEIPDCYTFSVLITFDNKAHSGRIPISLETQAHIOECK--HPSVFOHGDNSFRLLFDV 303

Db 272 RHQELPDCYDFTLTITFDNKAHSGRIKISLNDNISIKECDWHVSGSIQKXNTHYMMIFDA 331

QY 304 VVILTCSLFLLCARSLRGLLQNEFVGFWMRQRGRVISLWERLEFVNGWYILLVTSV 363

Db 332 FVILTCLASLVLCARSVIRGLQOQEFVNFLLHYKKEVSASDQMEFINGWYIMILSDI 391

QY 364 LTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGIRYLTFFHNYNILLATLRVALP 423

Db 392 LTIVGSVLKWEIOAKSLTSYDVCSILLGTSTMLVWLGVIRYLGFFAKYNLLILILQAAALP 451

QY 424 SVMRFCCCVAVIYLYGCFCGWIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFAMQAQ 483

Db 452 NVMRFCCCAAMIYLYGCFCGWIVLGPYHEKFRSLNRVSECLFSLINGDDMFSTFAKMQQ- 510

QY 484 QGRSSLVWLFSQLYLYSFISLFIYMWLSLFIALITGAYDTIKHPGGAGAESELOAYIAQ 543

Db 511 --KSYLVWLFSTRVYLYSFISLFIYMWLSLFIALITDTVETIKHYQQDGFPETELKFAIE 568

QY 544 CQDSPTSGKFRRGSGSACSLCC 567

Db	569	CKDLPNSGKYRLEDDAPGSLCC	592	
RESULT 7				
Q8R4F0				
ID	Q8R4F0	PRELIMINARY;	PRT;	553 AA.
AC	Q8R4F0;			
DT	01-JUN-2002	(Tremblrel. 21, Created)		
DT	01-JUN-2002	(Tremblrel. 21, Last sequence update)		
DT	01-MAR-2003	(Tremblrel. 23, Last annotation update)		
DE	Mucolipin-3.			
GN	MCOLN3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J;			
RC	MEDLINE=22317414; PubMed=12403827;			
RA	Di Palma F., Belyantseva I.A., Kim H.J., Vogt T.F., Kachar B.,			
RA	Noben-Trauth K.;			
RT	"Mutations in Mcoln3 associated with deafness and pigmentation defects			
RT	in varitint-waddler (Va) mice.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:14994-14999(2002).			
DR	EMBL; AF475086; AAL84623.1; -.			
DR	EMBL; AY083531; AAM08924.1; -.			
DR	MGD; MGI:1890500; Mcoln3.			
DR	InterPro; IPR002111; Cat_channel_TrpL.			
DR	InterPro; IPR005821; Ion_trans.			
DR	Pfam; PF00520; ion_trans; 1.			
KW	Ionic channel; Transmembrane.			
SQ	SEQUENCE 553 AA; 63748 MW; 8E257B05D96DF536 CRC64;			
Query Match 53.0%; Score 1626.5; DB 11; Length 553;				
Best Local Similarity 55.5%; Pred. No. 1.9e-136;				
Matches 313; Conservative 90; Mismatches 122; Indels 39; Gaps 6;				
Qy	7	PRGSETERLLTPNPGYGTQAGSPAPPTPPEEEDLRRLKYFFMSPCDKFRAGRKPKCL	66	
Db	24	PSSSPSEQLLL-----EDQMRRLKFFFFMNPCEKFWARGKPKWL	63	
Qy	67	MLQVVKILVTVQLILFGLSNQLAVTFRENTIAFRHLFLLGYSDGADDTFAAYTREQLY	126	
Db	64	AIQILKIAMVTIQLVFLGSLNQMVVAFKEENTIAFKHLFLKGYMDRMDDTYAVYTQSEVY	123	
Qy	127	QAIFHAVDQYLALPDVSLGRYAYVRGGDPWTNGSLALCQRYYHRGHVDPANDTFDIDP	186	
Db	124	DQIIFAVTQYLQLQNISVGNHAYENKG-----TKQSAMAICQHFYRQGTICPGNDTFDIDP	179	
Qy	187	MVVTDCIQVDPPEPPPPDDTLTLESSSSYK-NLTCLKFHLVNVTHFRLKTINLQSL	245	
Db	180	EVETECFLVEP-----DEASHLGTGPGENKLNLSDFHRLTLVELQFKLKAINLQTV	230	
Qy	246	INNEIPDCYTFSLITFDNKAHSGRIPISLETQAHIOECK--HPSVFQHGDNFRLFLDV	303	
Db	231	RHQLPDCYDFTLTITFDNKAHSGRIKISLDNDISIKECKDWHVSGSIQKNTHYMMIFDA	290	
Qy	304	VVILTCSLSFLLCARSLRGLLQNEFVGFMMRQGRVVISLWERLEFVNGWYILLVTSDV	363	
Db	291	FVILTCLASLVLCARSVIRGLQEQEFVNFLLHYKKEVSASDQMEFINGWYIMIIISDI	350	
Qy	364	LTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIYRLTFFHNNYINILATLRVALP	423	
Db	351	LTIVGSVLKMEIOAKSLTSYDVCSILLGTSTMLVWLGVIYRLGFFAKYNLLILTQAALP	410	
Query Match 53.0%; Score 1626.5; DB 11; Length 591;				
Best Local Similarity 55.5%; Pred. No. 2.1e-136;				
Matches 313; Conservative 90; Mismatches 122; Indels 39; Gaps 6;				
Qy	7	PRGSETERLLTPNPGYGTQAGSPAPPTPPEEEDLRRLKYFFMSPCDKFRAGRKPKCL	66	
Db	62	PSSSPSEQLLL-----EDQMRRLKFFFFMNPCEKFWARGKPKWL	101	
Qy	67	MLQVVKILVTVQLILFGLSNQLAVTFRENTIAFRHLFLLGYSDGADDTFAAYTREQLY	126	
Db	102	AIQILKIAMVTIQLVFLGSLNQMVVAFKEENTIAFKHLFLKGYMDRMDDTYAVYTQSEVY	161	
Qy	127	QAIFHAVDQYLALPDVSLGRYAYVRGGDPWTNGSLALCQRYYHRGHVDPANDTFDIDP	186	
Db	162	DQIIFAVTQYLQLQNISVGNHAYENKG-----TKQSAMAICQHFYRQGTICPGNDTFDIDP	217	
Qy	187	MVVTDCIQVDPPEPPPPDDTLTLESSSSYK-NLTCLKFHLVNVTHFRLKTINLQSL	245	
Db	218	EVETECFLVEP-----DEASHLGTGPGENKLNLSDFHRLTLVELQFKLKAINLQTV	268	
Qy	246	INNEIPDCYTFSLITFDNKAHSGRIPISLETQAHIOECK--HPSVFQHGDNFRLFLDV	303	
Db	269	RHQLPDCYDFTLTITFDNKAHSGRIKISLDNDISIKECKDWHVSGSIQKNTHYMMIFDA	328	
Qy	304	VVILTCSLSFLLCARSLRGLLQNEFVGFMMRQGRVVISLWERLEFVNGWYILLVTSDV	363	
Db	329	FVILTCLASLVLCARSVIRGLQEQEFVNFLLHYKKEVSASDQMEFINGWYIMIIISDI	388	
Qy	364	LTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIYRLTFFHNNYINILATLRVALP	423	
Db	389	LTIVGSVLKMEIOAKSLTSYDVCSILLGTSTMLVWLGVIYRLGFFAKYNLLILTQAALP	448	
Qy	424	SVMRFCCCVAVIYLGFCGWIIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFAMQAO	483	
Db	449	NVMRFCCCAAMIYLGFCGWIIVLGPYHVKFRSLNRVSECLFSLINGDDMFSTFAKMQQ-	507	

Qy	424	SVMRFCCCVAVIYLGFCGWIIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFAMQAO	483	
Db	411	NVMRFCCCAAMIYLGFCGWIIVLGPYHVKFRSLNRVSECLFSLINGDDMFSTFAKMQQ-	469	
Qy	484	QGRSSLVWLFSQLYLSFISLFIYMLVLSLFIALITGAYDTIKHPGGAGAESELSQAYIAQ	543	
Db	470	--KSYLVWLFSSRVLYLSFISLFIYMLSLFIALITDTYETIKHYQODGFPFTELKRFIAE	527	
Qy	544	CQDSPTSGKFRRGSGSACSLLCCC	567	
Db	528	CKDLPNSGKYRLEDDPPGSLCCC	551	
RESULT 8				
Q8BSG1				
ID	Q8BSG1	PRELIMINARY;	PRT;	591 AA.
AC	Q8BSG1;			
DT	01-MAR-2003	(Tremblrel. 23, Created)		
DT	01-MAR-2003	(Tremblrel. 23, Last sequence update)		
DT	01-MAR-2003	(Tremblrel. 23, Last annotation update)		
DE	Weakly similar to MUCOLIPIDIN (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Mesonephros;			
RC	MEDLINE=22354683; PubMed=12466851;			
RA	The FANTOM Consortium,			
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotation of			
RT	60,770 full-length cDNAs.";			
RL	Nature 420:563-573(2002).			
DR	EMBL; AK033008; BAC28123.1; -.			
FT	NON TER			
SQ	SEQUENCE 591 AA; 67954 MW; 2A3B53196F057268 CRC64;			
Query Match 53.0%; Score 1626.5; DB 11; Length 591;				
Best Local Similarity 55.5%; Pred. No. 2.1e-136;				
Matches 313; Conservative 90; Mismatches 122; Indels 39; Gaps 6;				
Qy	7	PRGSETERLLTPNPGYGTQAGSPAPPTPPEEEDLRRLKYFFMSPCDKFRAGRKPKCL	66	
Db	62	PSSSPSEQLLL-----EDQMRRLKFFFFMNPCEKFWARGKPKWL	101	
Qy	67	MLQVVKILVTVQLILFGLSNQLAVTFRENTIAFRHLFLLGYSDGADDTFAAYTREQLY	126	
Db	102	AIQILKIAMVTIQLVFLGSLNQMVVAFKEENTIAFKHLFLKGYMDRMDDTYAVYTQSEVY	161	
Qy	127	QAIFHAVDQYLALPDVSLGRYAYVRGGDPWTNGSLALCQRYYHRGHVDPANDTFDIDP	186	
Db	162	DQIIFAVTQYLQLQNISVGNHAYENKG-----TKQSAMAICQHFYRQGTICPGNDTFDIDP	217	
Qy	187	MVVTDCIQVDPPEPPPPDDTLTLESSSSYK-NLTCLKFHLVNVTHFRLKTINLQSL	245	
Db	218	EVETECFLVEP-----DEASHLGTGPGENKLNLSDFHRLTLVELQFKLKAINLQTV	268	
Qy	246	INNEIPDCYTFSLITFDNKAHSGRIPISLETQAHIOECK--HPSVFQHGDNFRLFLDV	303	
Db	269	RHQLPDCYDFTLTITFDNKAHSGRIKISLDNDISIKECKDWHVSGSIQKNTHYMMIFDA	328	
Qy	304	VVILTCSLSFLLCARSLRGLLQNEFVGFMMRQGRVVISLWERLEFVNGWYILLVTSDV	363	
Db	329	FVILTCLASLVLCARSVIRGLQEQEFVNFLLHYKKEVSASDQMEFINGWYIMIIISDI	388	
Qy	364	LTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIYRLTFFHNNYINILATLRVALP	423	
Db	389	LTIVGSVLKMEIOAKSLTSYDVCSILLGTSTMLVWLGVIYRLGFFAKYNLLILTQAALP	448	
Qy	424	SVMRFCCCVAVIYLGFCGWIIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFAMQAO	483	
Db	449	NVMRFCCCAAMIYLGFCGWIIVLGPYHVKFRSLNRVSECLFSLINGDDMFSTFAKMQQ-	507	

Db 551 C 551

RESULT 11

Q9NV09 PRELIMINARY; PRT; 497 AA.
ID Q9NV09; AC Q9NV09;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Hypothetical protein FLJ11006.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y., Oshima A.;
RT "NEDO human cDNA sequencing project."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK001868; BAA91951.1; -
DR InterPro; IPR002111; Cat_channel_TrpL.
DR Pfam; PF00520; Ion_trans; 1.
DR Hypothetical protein; Ionic channel; Transmembrane..
KW SEQUENCE 497 AA; 57739 MW; 3128395B50E5890D CRC64;

Query Match 45.5%; Score 1396; DB 4; Length 497;
Best Local Similarity 51.2%; Pred. No. 6.1e-116;
Matches 277; Conservative 78; Mismatches 108; Indels 78; Gaps 7;

QY 34 TPPEE-----DRLRLKYFFMSPCDKFRAGKPKCKMLQVVKILVTVQVQLILFGLSNQ 88
Db 26 TSPSEELLEQVRRKLLKFFMNPCEKFWARGKPKWKLAIQIKIAMVTI----- 75
QY 89 LAVTFRENTIAFRHLFLGYS DGADDTFAAYTREQLYQAFHVDQYLALPDVSLGRYA 148
Db 76 -----QYLQLYNVSVGNHA 89
QY 149 YVRGGDPWTNGSLALCQRYYHRGHVDPANDTFDIDPMVVTDCIQVDPPEPPPSDD 208
Db 90 YENKG---TKQSAVAICQHFYKRGNIYFGNDTFDIDPEIETECFFVEPDE-----PPhi 140
QY 209 LTLLESSSSYKNTLKFHKLNVNTIHERLKTINLQSLINNEIPDCYTFSLITFDNKAHS 268
Db 141 GTPAENK---LNLTLDFHRLTLTVELQFKLAINLQTVRHQELPDCYDFTLTITFDNKAHS 197
QY 269 GRIPISLETAHQIECK--HPSVFQHGDNFRLFLDQVVTLCSLFLLCARSLRGFLL 326
Db 198 GRIKISLNDISIRECKDWHVSGSIQKNTHYMMIFDAFVILTLCLVSLILCIRSVIRGLQL 257
QY 327 QNEFVGMWRQGRVVISLWERLEFVNGWYILLVTSVLTISGTMKIGIEAKNLASYDVC 386
Db 258 QQEFVNFLLHYKKEVSVSDQMEFVNGWYIMIIISDILTIICSLKMEIQAKSLTSYDVC 317
QY 387 SILLGSTLLVWGVIRYLTFFHNYNLIATLRVALPSVMRCCCVAVIYLYGFCGWIIV 446
Db 318 SILLGSTMLVWGVIRYLTGFFAKYNLLITLQAAALPNVIRPCCCAAMIYLYGFCGWIIV 377
QY 447 LGPYHVKFRSLMVSECLFSLINGDDMFVTFAMQAQQGRSSLVWLFSQLYLSFISLFI 506
Db 378 LGPYHDKFRSLMVSECLFSLINGDDMFATPAKMQQ---KSYLVWLFSLYLSFISLFI 434
QY 507 YMVLSLFIALITGAYDTIKHPGGAGAESELSQAYIAQCQDSPTSGKFRRGSGSACSLICC 566
Db 435 YMLSLFIALITDTYETIKYQQQDGFPELTFTFISECKDLNPSGKYRLEDPPVSLFCC 494

QY 567 C 567
Db 495 C 495

RESULT 12

Q8IZK6 PRELIMINARY; PRT; 538 AA.
ID Q8IZK6; AC Q8IZK6;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Mucolipin 2.
GN MCOLN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22317414; PubMed=12403827;
RA Di Palma P., Belyantseva I.A., Kim H.J., Vogt T.F., Kachar B.,
RA Noben-Trauth K.;
RT "Mutations in MCOLN3 associated with deafness and pigmentation defects
in varitint-waddler (Va) mice."
RL Proc. Natl. Acad. Sci. U.S.A. 99:14994-14999 (2002).
DR EMBL; AY083533; AAM08926.1; -
SQ SEQUENCE 538 AA; 62684 MW; 1BCCB92F8D6C83C4 CRC64;

Query Match 44.8%; Score 1374; DB 4; Length 538;
Best Local Similarity 48.9%; Pred. No. 6.2e-114;
Matches 268; Conservative 115; Mismatches 143; Indels 22; Gaps 8;

QY 37 EEEDLRRRLKYFFMSPCDKFRAGKPKCKMLQVVKILVTVQVQLILFGLSNQVAFREE 96
Db 9 KEECLREDLKFYFMSPCYKRRARQIPWKLGQLIKIVMTTQLVRFGLSNQVAFKED 68
QY 97 NTIAFRHLFLGYS DGADDTF--AAYTREQLYQAFHVDQYLALPDVSLGRYAVRGGG 154
Db 69 NTVAFKHLFLKGSYSGTDEDDYSCSVYTQEDAYESIFFAINQYHQLKDITLGLGY---G 124
QY 155 DPWTNGSLALCQRYYHRGHVDPANDTFDIDPMVVTDCIQVDPPEPPPSDDLTLES 214
Db 125 ENEDNRIGLVCKQHYKKGTMFPFNETLNIDNDVELDCVQLDQLDLSKXPPD-----WKN 179
QY 215 SSSYKNTLKFHKLNVNTIHERLKTINLQSLINNEIPDCYTFESVLITFDNKAHSGRIPIS 274
Db 180 SSFPR--LEFYELLOVEISFHLKGLDLOTIHSRELPCVVFQNTIIFDNKAHSGKIKY 236
QY 275 LETQAHIOECKHPSVF--QHGDNSFLLFDVVVILTCSLSFLLCARSLLRGFLNQEFVG 332
Db 237 FDSDAKIECKDLNIFGSGTQKNAQYVLVFPDAFVIVICLASLILCTRISIVLALRLKRFNL 296
QY 333 FMRQRGRVVISLWERLEFVNGWYILLVTSVLTISGTMKIGIEAKNLASYDVCISLLGT 392
Db 297 FFLEKYKRPVCTDQWEFINGWYVLVIISDLMTIIGSILKMEIKAKNLNTYDLSIFLGT 356
QY 393 STLLVWGVIRYLTFFHNYNLIATLRVALPSVMRCCCVAVIYLYGFCGWIIVLGPYHV 452
Db 357 STLLVWGVIRYLTGFFQAYNVILTNQASLPKVLRFACAGMIYLYGTFCGWIVLGPYHD 416
QY 453 KFRSLMVSECLFSLINGDDMFVTFAMQAQQGRSSLVWLFSQLYLSFISLFIYMWLSL 512
Db 417 KPENLNTVAECLFSLVNGDDMFATFA--QIQQ-KSILVWLFSLYLSFISLFIYMWLSL 473
QY 513 FIALITGAYDTIKHPGGAGAESELSQAYIAQCQDSPTSGKFRRGSGSACSLICCGRDPS 572
Db 474 FIALITDSYDTIKKFKQNGFPETDLQFLKES---SKEBYQKESAFSLCICRRRKR 530
QY 573 EEHSLLVN 580
Db 531 DDHLIPIS 538

QY	216	SSYKNTLTKFKHKLNVNTHFR	275
Db	178	AQTSFFRLDFYRLVQVDISF	237
QY	276	ETQAHIQECKHPSVFQHDNS	333
Db	238	NSEANIECKNMNIGSSTQ	297
QY	334	M---WRQGRVISLWERLEF	390
Db	298	FLEKYKQRCVGADQW---	354
QY	391	GTSTLLVWVGIRVLTFFH	450
Db	355	GTSTLFWVGIRVILCYFQ	414
QY	451	HVKPRSLMSVSECLSLNG	510
Db	415	HEKFENLNIVAECLFSLV	471
QY	511	SLFIALITGAYDTIKHPG	570
Db	472	SLFIALITDSYHTIKKYQ	528
QY	571	PSEHSLVN 580	
Db	529	RSNDHLID 538	

RESULT 14

Q8K595 PRELIMINARY; PRT; 566 AA.

Q8K595; 566 AA.

01-OCT-2002 (TrEMBLrel. 22, Created)

01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Mucolipin-2.

330002C04RIK OR MCOLN2.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.

STRAIN=C57BL/6J;

Kennedy J.C., Falardeau J.L., Acierno J.S. Jr., Slangenaupt S.A.;

Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

EMBL; AF503575; AAM28596.1; -.

MGD; MGI:191529; 3300002C04Rik.

InterPro; IPR002111; Cat_channel_TrpL.

SEQUENCE 566 AA; 65449 MW; 314CEC662B3BDC07 CRC64;

Query Match 43.5%; Score 1335; DB 11; Length 566;

Best Local Similarity 49.3%; Pred. No. 2e-110;

Matches 271; Conservative 101; Mismatches 150; Indels 28; Gaps 9;

QY	38	EEDLRRLKYFFMSPCDK	97
Db	38	EEDLRRLKYFFMSPCKE	97
QY	98	TIAFRHLFLGYSDGADTFAA	155
Db	98	TIAFRHLFLGYSDGADTFAA	153
QY	156	PWTNGSLGALCQRYH	215
Db	154	SEDNRTGLKVCKQHYKT	205
QY	216	SSYKNTLTKFKHKLNVNTHFR	275
Db	206	AQTSFFRLDFYRLVQVDISF	265
QY	276	ETQAHIQECKHPSVFQHDNS	333

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RESULT 13
Q9CQD3
ID Q9CQD3 PRELIMINARY; PRT; 538 AA.
AC Q9CQD3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE 3300002C04Rik protein (Mucolipin 2).
GN 3300002C04RIK OR MCOLN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo, and Embryonic liver;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner T., Gissi C., King B., Kochiwa H.,
RA Fleischmann W., Gaasterland T., Niki K., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Baldairelli R., Barsh G.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldairelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bernaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyoko-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cdna collection.";
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22317414; PubMed=12403827;
RA Di Palma F., Belyantseva I.A., Kim H.J., Vogt T.F., Kachar B.,
RA Noben-Trauth K.;
RT "Mutations in Mcoln3 associated with deafness and pigmentation defects
in varitint-waddler (Va) mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14994-14999(2002).
DR EMBL; AK019454; BAB31730.1; -
DR EMBL; AK014467; BAB29372.1; -
DR EMBL; AY083532; AAM08925.1; -
DR MGD; MGI:1915529; 3300002C04Rik.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00520; Ion_trans; 1.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 538 AA; 62269 MW; 9C35081FE96A628B CRC64;

Query Match 43.5%; Score 1335; DB 11; Length 538;
Best Local Similarity 49.3%; Pred. No. 1.9e-110;
Matches 271; Conservative 101; Mismatches 150; Indels 28; Gaps 9;

QY 38 EEDLRRRLKYPFMSPCDKFRAGKPKCKMLQVVKILVVTQVLIPLFGLSNQLAVTFREEN 97
DB 10 EECLREDLKYPFMSPCEKYRARRQIPWKLGLQILKIVMVTTQLVRFGLSNQLVAVFEDN 69
QY 98 TIAFRHLFLLCYSDGADDTFAA--YTREQLYQAIFFHAVDQYALPDVSLGRYAYVRGGD 155
DB 70 TVAFKHLFLKGFSGVDEDDYSCTYTQENTYESIFFAIKQYRHLKXNISLATLGY----GE 125
QY 156 PWTNGSGLALCQRYHRGHVDPANDTFDIDPMVVTDCIQVDPPERPPPSDDLTLESS 215
DB 126 SEDNRTGLKVKQHYKTGAMFSNETLNIDSDIETCDIHLDLQVLTTEP-----EDW 177

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Db 266 NSEANIECKNMNISGSGTQSTHYLLVDFVIMICLASLILCTRSIVLALRLKRFLNF 325
Qy 334 M---WRQGRVISLWERLEFVNGWVILLVTSVLTISGTMKIGIEAKNLSYDVCSILL 390
Db 326 FLEKYQRVCADQW---EFVNGWVYLVVTSIDMTIIGSILKMEIKAKLTNYDVCSILL 382
Qy 391 GTSTLLVWVGIVIRYLTFFHNYNLIATLRVALPSVNRFCVAVIYLYGFCGWIIVLGPY 450
Db 383 GTSTLFVWVGIVIRYLYGYFQTYNVLLTMOASLPKVLRFACAGMIYLYGYTCGWIIVLGPY 442
Qy 451 HVKFRSLMVSECLFSLINGDDMFVTFPAAQOQGRSSLVWLFSQLYLYSFISLFIYMV 510
Db 443 HEKFENLNIVAECLFSLVNGDDMEATFA--QIQQ-KSILVWLFSLYLYSFISLFIYMV 499
Qy 511 SLFIALITGAYDTIKHPGGAGAESELOAYIAQCQDSPTSGKFRRGSGSACSLCCCGRD 570
Db 500 SLFIALITDSYHTIKKYQHGFPEPDLQKFL--KESGSKDGYQKQPSALLSCLCCLRRR 556
Qy 571 PSEEHSLLVN 580
Db 557 RSNDDLILID 566
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RESULT 15

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Q8K2T6
ID Q8K2T6 PRELIMINARY; PRT; 538 AA.
AC Q8K2T6;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE RIKEN cDNA 3300002C04 gene.
GN 3300002C04RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029847; AAH29847.1;
DR MGD; MGI:1915529; 3300002C04RIK.
DR InterPro; IPR002111; Cat channel_TrpL.
SQ SEQUENCE 538 AA; 62296 MW; 861C081FE96A628B CRC64;
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Query Match 43.4%; Score 1332; DB 11; Length 538;
Best Local Similarity 49.1%; Pred. No. 3.5e-110;
Matches 270; Conservative 102; Mismatches 150; Indels 28; Gaps 9;

Qy 38 EEDLRRRLKYFFMSPCKFRAGKPKCKMLQWVKILVTVQILFGLSNQLAVTFREEN 97
Db 10 EEDLREDLKFFMSPCKYRARRQIPWKLGILKIVMTTQLVRFGLSNQLVVAPEKN 69

Qy 98 TIAPRHLFLGYSDGADDTFAA--YTRQLYQAIFHAVDQYLALPDVSLGRYAYVRGGGD 155
Db 70 TVAFKHLFLKGFSGVDEDDYSCSIYTOENTYSEIFFAIKQYRLKNISLATLGY----GE 125

Qy 156 PWTNGSLALCQRYVHRGHVDPANDTFIDPMVVTDCIQVDPPEPPPPPPSDDLTLLESS 215
Db 126 SEDNRTGLKVCKQHYKGTGAMFSSNETLNIDSDIETDCIHLDLQVLITTEP-----EDW 177

Qy 216 SSYKNLTLKFKHLNVNTHFRKLTINLQSLINNEIPDCYTFPSVLITFDNKAHSGRIPI 275
Db 178 AQTSFPRDLDFYRLVQVDISFALKGIDLQAVHSREIPDCYLFQNTITFDNTAHSKIKIYL 237

Qy 276 ETOAHIQECKHPSVFGHGDNS--FRLLFDVVVILTCSLSLFLLCARSLRGLLQNEFVGF 333
Db 238 NSEANIECKNMNISGSGTQSTHYLLVDFVIMICLASLILCTRSIVLALRLKRFLNF 297

Qy 334 M---WRQGRVISLWERLEFVNGWVILLVTSVLTISGTMKIGIEAKNLSYDVCSILL 390
Db 298 FLEKYQRVCADQW---EFVNGWVYLVVTSIDMTIIGSILKMEIKAKLTNYDVCSILL 354
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Search completed: October 27, 2003, 18:06:14
Job time : 96 secs

GenCore version 5.1.6
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OMprotein - protein search, using sw model

Run on: October 27, 2003, 12:34:37 ; Search time 75 Seconds
(without alignments)
1227.485 Million cell updates/sec

Title: US-09-851-494B-3
Perfect score: 3067
Sequence: 1 MTAPAGPRGSETERLLTPNP.....CSLLCCCGRDFSEHSLLVN 580

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3067	100.0	580	AAB74707	Human membrane ass
2	3067	100.0	580	ABB07816	Human TLCC-2 prote
3	3067	100.0	580	AAM51858	Human TRP-like cal
4	2685	87.5	511	ABB89949	Human polypeptide
5	2661	86.8	511	AAB08906	Human secreted pro
6	1396	45.5	497	AAB93412	Human protein sequ
7	1376	44.9	538	ABU12053	Human NOV9c CG9070
8	1368	44.6	566	ABU12054	Human NOV9d CG9070
9	1367	44.6	544	ABU12052	Human NOV9b CG9070

10	1311	42.7	540	24	ABU12051	Human NOV9a CG9070
11	1226	40.0	255	23	ABB72389	Murine protein iso
12	1025.5	33.4	652	22	ABB71675	Drosophila melanog
13	979	31.9	191	22	ABG01744	Novel human diagn
14	689	22.5	193	22	AAU00503	Human TANGO 480 pr
15	627	20.4	154	23	ABB89290	Human polypeptide
16	599.5	19.5	164	22	ABB11279	Human secreted pro
17	551	18.0	600	22	ABG01746	Novel human diagn
18	507.5	16.5	106	22	ABG25123	Novel human diagn
19	308	10.0	1120	22	ABG25135	Novel human diagn
20	293	9.6	603	22	ABG27454	Novel human diagn
21	281.5	9.2	69	22	ABG57092	Human liver peptid
22	281.5	9.2	69	22	AAM63524	Human brain expres
23	281.5	9.2	69	22	AAM35448	Peptide #9485 enco
24	259.5	8.5	120	22	AAM89441	Human immune/haema
25	207.5	6.8	642	22	ABG08087	Novel human diagn
26	161.5	5.3	897	22	ABB62418	Drosophila melanog
27	152.5	5.0	621	23	AAU98515	Mouse Polycystin-2
28	152.5	5.0	966	23	ABO7819	Mouse polycystic k
29	152.5	5.0	966	23	AAM51861	Murine polycystic
30	150.5	4.9	76	22	ABG58066	Human liver peptid
31	150.5	4.9	76	22	ABB42654	Peptide #10160 enc
32	150.5	4.9	76	22	ABB25997	Protein #7996 enco
33	150.5	4.9	76	22	AAM63544	Human bone marrow
34	150.5	4.9	76	22	AAM76359	Human brain expres
35	150.5	4.9	76	22	AAM36467	Peptide #10504 enc
36	150.5	4.9	76	23	ABG45651	Human peptide enco
37	147.5	4.8	2253	21	AAV44301	Human acrosome rea
38	146	4.8	469	22	AAM41866	Human polypeptide
39	141.5	4.6	224	22	AAM31154	Peptide #5191 enco
40	140.5	4.6	805	23	AAE25587	Human polycystic k
41	140	4.6	2126	21	AAV44302	Mouse acrosome rea
42	138	4.5	866	22	AAB68448	Amino acid sequenc
43	136.5	4.5	805	21	AAV70245	Human Polycystin-L
44	127	4.1	53	22	ABG56654	Human liver peptid
45	127	4.1	53	22	ABB41211	Peptide #8717 enco

ALIGNMENTS

RESULT 1
AAB74707
ID AAB74707 standard; Protein; 580 AA.
XX
AC AAB74707;
XX
DT 12-JUN-2001 (first entry)
XX
DE Human membrane associated protein MEMAP-13.
XX
KW Human; membrane associated protein; MEMAP; diagnosis; cytostatic;
KW antiinflammatory; anticonvulsant; immunosuppressive; antidiarrheic;
KW antiarteriosclerotic; gene therapy; cell proliferative disorder;
KW autoimmune disorder; inflammatory disorder; neurological disorder;
KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;
KW epilepsy; diarrhoea.
XX
OS Homo sapiens.
XX
PN WO200112662-A2.
XX
PD 22-FEB-2001.
XX
PF 14-AUG-2000; 2000WO-US22315.
XX
PR 17-AUG-1999; 99US-0149641.
PR 09-NOV-1999; 99US-0164203.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;
Baughn MR, Lu DAM, Patterson C;

XX WPI; 2001-168860/17.
DR N-PSDB; AAF81753.
DR
XX
PT Isolated polypeptide with a human membrane associated protein sequence
PT is useful for the diagnosis, prevention and treatment of cell
PT proliferative, autoimmune/inflammatory, neurological and
PT gastrointestinal disorders -
XX
XX
XX Claim 1; Page 125-126; 173pp; English.
XX
CC AAF81741 to AAF81777 encode the human membrane associated proteins
CC (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,
CC antiinflammatory, anticonvulsant, immunosuppressive, antidiarrheic and
CC antiarteriosclerotic activities, which can be used in gene therapy.
CC MEMAPs and agonist of MEMAPs can be used to treat a disease or condition
CC associated with decreased expression of functional MEMAP and antagonists
CC of MEMAP are used to treat a disease or condition associated with
CC overexpression of functional MEMAP. These disorders include cell
CC proliferative, autoimmune/inflammatory, neurological and gastrointestinal
CC disorders. The MEMAP polynucleotides and proteins are also used for the
CC diagnosis of these disorders. Specific examples of these disorders
CC include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea.
CC MEMAP proteins can be used to screen for compounds which specifically
CC bind MEMAP including antibodies, oligonucleotides, proteins and small
CC molecules. MEMAP polynucleotides can be used to prepare transgenic
CC animals which can be studied to provide information concerning human
CC disease. Anti-MEMAP antibodies are useful in immunoassays for the
CC detection of MEMAP protein and can be used as antagonists to treat or
CC prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
CC can be delivered to target cells with genetic abnormalities with respect
CC to the expression of MEMAP to treat or prevent a disorder associated
CC with MEMAP.
XX
SQ Sequence 580 AA;

Query Match 100.0%; Score 3067; DB 22; Length 580;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTAPAGPRGSETERLLTPNPGYGTQAGSPAPPTPEEDLRRRLKYFFMSPCDKFRAG 60
DB 1 MTAPAGPRGSETERLLTPNPGYGTQAGSPAPPTPEEDLRRRLKYFFMSPCDKFRAG 60

QY 61 RKPKKMLQVVKILVTVQLILFLGLSNQLAVTPEENTIAFRHLFLGYSGDADDTFAAY 120
DB 61 RKPKKMLQVVKILVTVQLILFLGLSNQLAVTPEENTIAFRHLFLGYSGDADDTFAAY 120

QY 121 TREQLYQAIHFAVDQYLALPDVSLGRYAYVRGGDPWTNGSLALCORYYHRGHVDPAND 180
DB 121 TREQLYQAIHFAVDQYLALPDVSLGRYAYVRGGDPWTNGSLALCORYYHRGHVDPAND 180

QY 181 TFDIDPMVVTDCIQVDPERPPPPDDLTLLSSSSYKNLTKEHLVNVTHFRLXTI 240
DB 181 TFDIDPMVVTDCIQVDPERPPPPDDLTLLSSSSYKNLTKEHLVNVTHFRLXTI 240

QY 241 NLQSLINNEIPDCYTFESVLITFDNKAHSGRIPISLETQAHIOECKHPSVFQHGDNFSRL 300
DB 241 NLQSLINNEIPDCYTFESVLITFDNKAHSGRIPISLETQAHIOECKHPSVFQHGDNFSRL 300

QY 301 FDVVVILTCSLSFLLCARSLRGLFLLQNEFVGFMWRQGRVISLWERLEFVNGWYILLVT 360
DB 301 FDVVVILTCSLSFLLCARSLRGLFLLQNEFVGFMWRQGRVISLWERLEFVNGWYILLVT 360

QY 361 SDVLTISGTMKIGIEAKNLASYDVCSILLGTSTLLVWVGIVRYLTFFHNNILIATLRV 420
DB 361 SDVLTISGTMKIGIEAKNLASYDVCSILLGTSTLLVWVGIVRYLTFFHNNILIATLRV 420

QY 421 ALPSVMRFCCCAVIVLYGCFCCGIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFAM 480
DB 421 ALPSVMRFCCCAVIVLYGCFCCGIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFAM 480

QY 481 QAQGRSSLVWLFSQLYLSFISLFYVWLSLFIALITGAYDTIKHPGGAGAESELOAY 540

DB 481 QAQGRSSLVWLFSQLYLSFISLFYVWLSLFIALITGAYDTIKHPGGAGAESELOAY 540
QY 541 IAQCQDSPTSGKFRGSGSACSLCCCGRDPSEHSLLVN 580
DB 541 IAQCQDSPTSGKFRGSGSACSLCCCGRDPSEHSLLVN 580

RESULT 2
ABB07816
ID ABB07816 standard; Protein; 580 AA.
XX
AC ABB07816;
XX
DT 03-JUL-2002 (first entry)
XX
DE Human TLCC-2 protein.
XX
KW Transient receptor potential like calcium channel; TRP; TLCC-2; human;
KW neuroprotective; analgesic; nootropic; antiparkinsonian; antidepressant;
KW cerebroprotective; anxiolytic; antimanic; anticonvulsant; gene therapy;
KW calcium signaling.
XX
OS Homo sapiens.
XX
PN US2002035056-A1.
XX
PD 21-MAR-2002.
XX
PF 06-APR-2001; 2001US-0828466.
XX
PR 07-APR-2000; 2000US-0544797.
XX
PA (CURT/) CURTIS R A J.
PA (SILO/) SILOS-SANTIAGO I.
XX
PI Curtis RAJ, Silos-Santiago I;
XX
DR WPI; 2002-338931/37.
DR N-PSDB; ABL40754, ABL40755.
XX
PT New nucleic acid designated TLCC-2 encodes a transient receptor
PT potential-like calcium channel and is useful to diagnose and treat pain
PT disorders and central nervous system neurodegenerative and neurological
PT disorders -
PS Claim 7; Fig 1A-B; 70pp; English.
XX
CC The invention relates to a novel transient receptor potential (TRP)-like
CC calcium channel, designated TLCC-2 and polynucleotides encoding the
CC TLCC-2. TLCC-2 can be expressed by standard recombinant methodology. The
CC TLCC-2 polypeptide, polynucleotides and modulators are useful for
CC treating central nervous system disorders such as neurodegenerative
CC disorders for example Alzheimer's disease, Parkinson's disease, multiple
CC sclerosis, amyotrophic lateral sclerosis, progressive supranuclear palsy,
CC epilepsy, Creutzfeldt-Jakob disease, AIDS-related dementia, familial
CC infantile convulsions, paroxysmal choreoathetosis, psychiatric disorders
CC such as depression, anxiety, schizophrenia, psychoses, mania or phobic
CC disorders, learning or memory disorders such as amnesia, age-related
CC memory loss, or a neurological disorder such as migraine. The molecules
CC are also useful to treat a pain disorder. The present sequence represents
CC the human TLCC-2 polypeptide.
XX
SQ Sequence 580 AA;

Query Match 100.0%; Score 3067; DB 23; Length 580;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTAPAGPRGSETERLLTPNPGYGTQAGSPAPPTPEEDLRRRLKYFFMSPCDKFRAG 60
DB 1 MTAPAGPRGSETERLLTPNPGYGTQAGSPAPPTPEEDLRRRLKYFFMSPCDKFRAG 60

Db 378 LGPYHDKFSLNMVSECLFSLNGDDMFATFAKMQQ--KSYLVWLFSLRIYLSFISLFI 434

Qy 507 YMVLSLFIALITGAYDTIKHPGGAGAESELOQAYIAQCQDSPSGKFRGSGSACSLCC 566

Db 435 YMILSLFIALITTYETIKQYQDGFPELRTFISECKDLNSGKYRLEDPPVSLFCC 494

Qy 567 C 567

Db 495 C 495

RESULT 7

ABU12053

ID ABU12053 standard; Protein; 538 AA.

XX

AC ABU12053;

XX

DT 19-FEB-2003 (first entry)

XX

DE Human NOV9c CG90709-03 protein SEQ ID 26.

XX

KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic; metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;

KW antilipaeamic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;

KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;

KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;

KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;

KW metabolic syndrome X; wasting disease.

XX

OS Homo sapiens.

XX

PN WO200281625-A2.

XX

PD 17-OCT-2002.

XX

PF 03-APR-2002; 2002WO-US10366.

XX

PR 03-APR-2001; 2001US-281086P.

PR 05-APR-2001; 2001US-281906P.

PR 06-APR-2001; 2001US-282020P.

PR 10-APR-2001; 2001US-282930P.

PR 12-APR-2001; 2001US-283444P.

PR 12-APR-2001; 2001US-283512P.

PR 13-APR-2001; 2001US-283657P.

PR 13-APR-2001; 2001US-283678P.

PR 13-APR-2001; 2001US-283710P.

PR 17-APR-2001; 2001US-284234P.

PR 19-APR-2001; 2001US-285325P.

PR 20-APR-2001; 2001US-285381P.

PR 24-APR-2001; 2001US-286068P.

PR 25-APR-2001; 2001US-286292P.

PR 07-JUN-2001; 2001US-296692P.

PR 26-JUN-2001; 2001US-300883P.

PR 08-AUG-2001; 2001US-311003P.

PR 13-AUG-2001; 2001US-311973P.

PR 16-AUG-2001; 2001US-312901P.

PR 14-SEP-2001; 2001US-322283P.

PR 05-OCT-2001; 2001US-327448P.

PR 31-DEC-2001; 2001US-345734P.

PR 03-JAN-2002; 2002US-345755P.

PR 04-FEB-2002; 2002US-354391P.

PR 02-APR-2002; 2002US-0114153.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Padigar M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD, Smithson G;

PI Guo X, Gerlach V, Casman SJ, Boldog FL, Li L, Zerhusen BD;

PI Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA, Malyankar UM;

PI Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J, Peyman JA;

PI Catterton E, MacDougall JR, Edinger SR, Stone DJ, Mazur A;

XX WPI; 2003-046862/04.

DR N-PSDB; ABX56273.

XX

PT New isolated NOVX polypeptide useful for treating cardiomyopathy,

PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious

PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and

PT cancer

XX

PS Claim 1; Page 112; 425pp; English.

XX

CC This invention describes novel polypeptides, termed NOVX which have

CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,

CC neuroprotective, antiparkinsonian, antilipaeamic, cytostatic, nootropic,

CC cardiant and immunomodulatory activity. The polypeptide and any

CC antibodies generated from it are useful in the manufacture of a

CC medicament for treating a syndrome associated with a human disease

CC selected from a pathology associated with the NOVX polypeptide. Fragments

CC and portions of the polynucleotides encoding NOVX polypeptides are useful

CC to map the location of NOVX genes on a chromosome, to identify

CC individuals from minute biological samples, as DNA markers for

CC restriction fragment length polymorphism (RFLP), and are useful to

CC prepare polymerase chain reaction primers. The products of the invention

CC can be used in gene therapy and for treating cardiomyopathy, metabolic

CC disorders, diabetes, atherosclerosis, obesity, infectious disease,

CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's

CC disease, immune disorders, haematopoietic disorders, and various

CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic

CC syndrome X and wasting disorders associated with chronic diseases and

CC various cancers. ABU12041-ABU12086 represent the polypeptide fragments

CC encoded by the NOVX polynucleotides represented in ABX56261-ABX56306.

XX

SQ Sequence 538 AA;

Query Match 44.9%; Score 1376; DB 24; Length 538;

Best Local Similarity 48.9%; Pred. No. 2e-139;

Matches 268; Conservative 115; Mismatches 143; Indels 22; Gaps 8;

Qy 37 EEDLRRRLKYFFMSPCDKPRAKRKPCKLMQVVKILVTVQLILFGLSNQLAVTFREE 96

Db 9 KEECLREDLKFFYMSPCEKYRARRQIPWKLGLQILKIVMVTTLQVRFGLSNQLVAFKED 68

Qy 97 NTIAPRHLFLLGYSDGADDTF--AAYTREQLYQAFHADVQYALPDVSLGRYAYVRGG 154

Db 69 NTVAFKHLFLKGYSGTDEDDYSCSVYTOEDAYESIFFAINQYHQLKDITLGLGY---G 124

Qy 155 DPWTNGSGLALCQRYHRGHVDPANDTFIDPMVWVILTCSLFLLCARSLRGLLQNEFVG 332

Db 125 ENEDNRIGLVCKVCKYKGTMTFSPNETLNDVDELDCVQLDLQSLKPPD----WKN 179

Qy 215 SSSYKNLTLKFHKLNVNVTIHFRLKTNLQSLINNEIPDCYTFSVLTFDNKAHSGRIPIS 274

Db 180 SSFFR--LEFYRLQVEISFHLKGIDLQTIHSRELPCYVFQNTIIFDNKAHSGKIKIY 236

Qy 275 LETQAHIQECKHPSVFOHGDNS--FRLLFDVWVILTCSLFLLCARSLRGLLQNEFVG 332

Db 237 FDSDAKIEECKDLNIFGSAQNAQYVLVDFAFVIVICLASLILCTRISIVLALRLKRFLN 296

Qy 333 FMRQRGRVISLWERLEFVNGWYILLVTSVDLTISGTIMKIGIEAKNLASYDVCISLLGT 392

Db 297 FFLEKYKRPVCDTDQWEFINGWYVLVVISDLMTIIGSILKWEIKAKNLNTYDLCSIFLGT 356

Qy 393 STLLVWVGVIYLTFFHNYNIIATLRVALPSVMRFOCCVAVIYLYGCFCGWIVLGPYHV 452

Db 357 STLLVWVGVIYLYGYFOAYNVILTMQASLPKVLRFACAGMIYLTGTCGWIIVLGPYHD 416

Qy 453 KFRSLSMVSECLFSLINGDDMFVTPAAMQAQQRRSSLVMLFSQLYLYSFISLFIYVLISL 512

Db 417 KFENLNTVAECLFSLVNGDDMFATFA--QIQQ-KSILVWLFSLRYLYSFISLFIYVLISL 473

Qy 513 FIALITGAYDTIKHPGGAGAESELOQAYIAQCQDSPSGKFRGSGSACSLCCGRDPS 572

Db 474 FIALITDSYDTIKKFFQONGFPETDLQEFLEKCS---SKEEYQKESAFSLCICRRRKRS 530

Qy 573 EEHSLLVN 580

Db 531 DDHLIPIS 538

RESULT 8
ABU12054

ID ABU12054 standard; Protein; 566 AA.
XX
AC ABU12054;
XX
DT 19-FEB-2003 (first entry)
XX
DE Human NOV9d CG90709-04 protein SEQ ID 28.
XX
KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
KW antilipemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
KW metabolic syndrome X; wasting disease.
XX
OS Homo sapiens.
XX
PN WO200281625-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US10366.
XX
PR 03-APR-2001; 2001US-281086P.
PR 05-APR-2001; 2001US-281906P.
PR 06-APR-2001; 2001US-282020P.
PR 10-APR-2001; 2001US-282930P.
PR 12-APR-2001; 2001US-283444P.
PR 12-APR-2001; 2001US-283512P.
PR 13-APR-2001; 2001US-283657P.
PR 13-APR-2001; 2001US-283678P.
PR 13-APR-2001; 2001US-283710P.
PR 17-APR-2001; 2001US-284234P.
PR 19-APR-2001; 2001US-285325P.
PR 20-APR-2001; 2001US-285381P.
PR 24-APR-2001; 2001US-286068P.
PR 25-APR-2001; 2001US-286292P.
PR 07-JUN-2001; 2001US-296692P.
PR 26-JUN-2001; 2001US-300883P.
PR 08-AUG-2001; 2001US-311003P.
PR 13-AUG-2001; 2001US-311973P.
PR 16-AUG-2001; 2001US-312901P.
PR 14-SEP-2001; 2001US-322283P.
PR 05-OCT-2001; 2001US-327448P.
PR 31-DEC-2001; 2001US-345734P.
PR 03-JAN-2002; 2002US-345755P.
PR 04-FEB-2002; 2002US-354391P.
PR 02-APR-2002; 2002US-0114153.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigaru M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD, Smithson G;
PI Guo X, Gerlach V, Casman SJ, Boldog FL, Li L, Zerhusen BD;
PI Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA, Malyankar UM;
PI Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J, Peyman JA;
PI Catterton E, MacDougall JR, Edinger SR, Stone DJ, Mazur A;
XX
DR WPI; 2003-046862/04.
DR N-PSDB; ABX56274.
XX
PT New isolated NOVX polypeptide useful for treating cardiomyopathy,
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT cancer -
XX
PS Claim 1; Page 113; 425pp; English.

KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
KW parkinson's disease; haematopoietic disorder; metabolic disturbance;
KW metabolic syndrome X; wasting disease.
XX

OS Homo sapiens.

PN WO200281635-A2.

XX 17-OCT-2002.

PF 03-APR-2002; 2002WO-US10366.

XX 03-APR-2001; 2001US-281086P.

PR 05-APR-2001; 2001US-281906P.

PR 06-APR-2001; 2001US-282020P.

PR 10-APR-2001; 2001US-282930P.

PR 12-APR-2001; 2001US-283444P.

PR 12-APR-2001; 2001US-283512P.

PR 13-APR-2001; 2001US-283657P.

PR 13-APR-2001; 2001US-283678P.

PR 13-APR-2001; 2001US-283710P.

PR 17-APR-2001; 2001US-284234P.

PR 19-APR-2001; 2001US-285325P.

PR 20-APR-2001; 2001US-285381P.

PR 24-APR-2001; 2001US-286068P.

PR 25-APR-2001; 2001US-286292P.

PR 07-JUN-2001; 2001US-296692P.

PR 26-JUN-2001; 2001US-300883P.

PR 08-AUG-2001; 2001US-311003P.

PR 13-AUG-2001; 2001US-311973P.

PR 16-AUG-2001; 2001US-312901P.

PR 14-SEP-2001; 2001US-322283P.

PR 05-OCT-2001; 2001US-327448P.

PR 31-DEC-2001; 2001US-345734P.

PR 03-JAN-2002; 2002US-345755P.

PR 04-FEB-2002; 2002US-354391P.

PR 02-APR-2002; 2002US-0114153.

XX (CURA-) CURAGEN CORP.

PA Padigaru M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD, Smithson G;

XX Guo X, Gerlach V, Casman SJ, Boldog FL, Li L, Zerhusen BD;

PI Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA, Malyankar UM;

PI Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J, Peyman JA;

PI Catterton E, MacDougall JR, Edinger SR, Stone DJ, Mazur A;

XX WPI; 2003-046862/04.

DR N-PSDB; ABX56271.

XX New isolated NOVX polypeptide useful for treating cardiomyopathy,

PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious

PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and

PT cancer -

XX Claim 1; Page 110; 425pp; English.

PS This invention describes novel polypeptides, termed NOVX which have

XX antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,

CC neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,

CC cardiant and immunomodulatory activity. The polypeptide and any

CC antibodies generated from it are useful in the manufacture of a

CC medicament for treating a syndrome associated with a human disease

CC selected from a pathology associated with the NOVX polypeptide. Fragments

CC and portions of the polynucleotides encoding NOVX polypeptides are useful

CC to map the location of NOVX genes on a chromosome, to identify

CC individuals from minute biological samples, as DNA markers for

CC restriction fragment length polymorphism (RFLP), and are useful to

CC prepare polymerase chain reaction primers. The products of the invention

CC can be used in gene therapy and for treating cardiomyopathy, metabolic

CC disorders, diabetes, atherosclerosis, obesity, infectious disease,

CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's

CC disease, immune disorders, haematopoietic disorders, and various

CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic

CC syndrome X and wasting disorders associated with chronic diseases and

CC various cancers. ABU12041-ABU12086 represent the polypeptide fragments

CC encoded by the NOVX polynucleotides represented in ABX56261-ABX56306.

XX

SQ Sequence 540 AA;

Query Match 42.7%; Score 1311; DB 24; Length 540;

Best Local Similarity 48.0%; Pred. No. 2.2e-132;

Matches 264; Conservative 110; Mismatches 144; Indels 32; Gaps 9;

QY 37 EEEDLRRRLKYFFMSPCDKFRAGKRPCKLMQVVKILVVTQVLILFGLSNQLAVTFREE 96

Db 9 KEECLREDLKFYFMSPCYKRAPQIPWKLGLQILKIVMTTQLVRFGLSNQLVFAFKED 68

QY 97 NTIAFRHLFLLGYSDGADDTF--AAYTREQLYQAFHVAVDQYLALPDVSLGRYAYVRGGG 154

Db 69 NTVAFKHLFLKGYSGTDEDDYSCSVYTQEDAYESIFFAINQYHQLKDITLGTLY---G 124

QY 155 DPWTNGSGLALCQRYHRGHVDPANDTFDIDPMVVTDCIQVDPPEPPPPDDDLTLLES 214

Db 125 ENEDNRIGLVCKQHYKKGTMPPSNETLNDVDELNCGVV-----AIYILKC 172

QY 215 SSSYKNLTGK----FHKLVNVTIHERLKTINLQSLINNEIPDCYFSLITFDNKAHSG 269

Db 173 YSLRDMITVTQYILFRLLQVEISFHLKGLDQLQTIHSRELPDCYVFQNTIIFDNKAHSG 232

QY 270 RIPISLETAHQIECKHPSVFQHGDNFRLLFDVVVILTCSLSFLLCARSLLRGFLQNE 329

Db 233 KIKIYFSDAKIEECKDLNIF--GSSKYALVFDAFVIVICLASLILCTRSIVLALRLR-R 289

QY 330 FVGFMWRQGRVISLWERLEFVNGWVILLVTSVLTISGTIMKIGIEAKNLASYDVCSIL 389

Db 290 FLNFFLEKYKRPVCDTDQWEFINGWVYLVIIISDLMTIIGSILKMEIKAKNLTYDLCSIF 349

QY 390 LGTSTLLVWVGVIYRLTFFHNYNILIALRLVALPSVMRFCCCVAVIYLGFCGIVLGP 449

Db 350 LGTSTLLVWVGVIYRLGYFOAYNVILTMQASLPKVLRFACAGMIYLGTYTFCGWIVLGP 409

QY 450 YHVFRSLSMVSECLFSLINGDDMFVTFAAMQAQGRSSLVWLFSQLYLYSFISLFIVMV 509

Db 410 YHLQFENLNTVAECLFSLVNGDDMFATFA--QIQQ-KSILVWLFSLYLYSFISLFIVMI 466

QY 510 LSLFIALITGAYDTIKHPGGAGAESELOQAYIAQCQDSPTSGKFRRGSGSACSLCCCR 569

Db 467 LSLFIALITDSYDTIKKQQNGFPETDLQEFLEKCS---SKEEYQKESSAFLSCICRRR 523

RESULT 11

ABB72389

ID ABB72389 standard; Protein; 255 AA.

XX

AC ABB72389;

XX

DT 04-APR-2002 (first entry)

XX

DE Murine protein isolated from skin cells SEQ ID NO: 713.

XX

KW Human; rat; mouse; skin cell; skin wound; cancer; growth defect;

KW developmental defect; inflammatory disease; dermatological; vulnery;

KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective.

XX

OS Mus sp.

XX WO200190357-A1.

XX 29-NOV-2001.

XX

PF 24-MAY-2001; 2001WO-NZ00099.
XX
PR 24-MAY-2000; 2000US-206650P.
FR 25-JUL-2000; 2000US-221232P.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD;
XX
DR WPI; 2002-122020/16.
DR N-PSDB; ABL35079.
XX
PT New polynucleotides and polypeptides encoded by the polynucleotides
PT isolated from skin cells, useful for treating skin wounds, cancers,
PT growth and developmental defects, inflammatory diseases, or for
PT modulating immune responses -
XX
PS Claim 4; Page 455; 466pp; English.
XX
CC The present invention provides the protein and coding sequences of cDNAs
CC isolated from human, murine and rat skin cell libraries. The sequences
CC can be used in the development of therapeutic agents useful in the
CC treatment of skin diseases, including skin wounds, cancer, growth
CC defects, developmental defects and inflammatory diseases. The proteins
CC have important roles in the induction of hair growth, cell proliferation
CC and cell-cell interaction, in maintaining tissue integrity, in wound
CC healing and in modulating immune responses. The present sequence is a
CC polypeptide of the invention.
XX
SQ Sequence 255 AA;
Query Match 40.0%; Score 1226; DB 23; Length 255;
Best Local Similarity 89.7%; Pred. No. 1.1e-123;
Matches 227; Conservative 13; Mismatches 13; Indels 0; Gaps 0;
QY 37 EEEDLRRRLKYFFMSPCDKFRAGRKPKCKMLQVVKILVVTQVQLIFGLSNQLAVTFREE 96
Db 1 EEEDLRRRLKYFFMSPCDKFRAGRKPKCKMLQVVKILVVTQVQLIFGLSNQLAVTFREE 60
QY 97 NTIAFRHLFLGYSDDGADDTFAAYTREQLYQAIHFAVDQYLALPDVSLGRYAYVRGGDP 156
Db 61 NTIAFRHLFLGYSDDGADDTFAAYTREQLYQAIHFAVDQYLALPDVSLGRYAYVRGGDP 120
QY 157 WTNGSLALCQRYHGHVDPANDTFDIDPMVVTDCIQVDPPPPPPPPSDDLTLLESSS 216
Db 121 WANGSALALCQRYHGHVDPANDTFDIDPMVVTDCIQVDPPPPPPPPSDDLTLLESSS 180
QY 217 SYKNLTALKFKHLVNTIHFRLKTIINQSLINNEIPDCYTFSLITFDNKAHSGRIPISLE 276
Db 181 SYKNLTALKFKHLVNTIHFRLKTIINQSLINNEIPDCYTFSLITFDNKAHSGRIPISLE 240
QY 277 TQAHIQECKHPSV 289
Db 241 TKTHIQECKHPSV 253
RESULT 12
ABB71675
ID ABB71675 standard; Protein; 652 AA.
XX
AC ABB71675;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 41817.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX

PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
DR N-PSDB; ABL15778.
DR
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
PT
XX Disclosure; SEQ ID NO 41817; 21pp + Sequence Listing; English.
PS
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 652 AA;
Query Match 33.4%; Score 1025.5; DB 22; Length 652;
Best Local Similarity 37.3%; Pred. No. 2.4e-101;
Matches 233; Conservative 119; Mismatches 190; Indels 83; Gaps 19;
QY 2 TAPAGPRGSETERLLTPNGYGTQAGSPAPPT-----PPE-----EEDLRRRL 45
Db 51 STPVAP-----VVEPMP---ISAGSGTAPPSVDGREGPEFPGSSAASYQEEERMRKL 99
QY 46 KYFFMSPCDKFRAGRKPKCKMLQVVKILVVTQVQLIFGLSNQLAVTFREENTIAFRHLF 105
Db 100 QFFFMNPIEKWQAKRKPKPKYFVVQIVKIFLVTMQLCLFAHSRYNHINYTGDNRFAPSHLF 159
QY 106 LLGYSDG-----ADDTFAAYTREQLYQAIHFAVDQYLALPDVSLGRYAYVRGGDPW 157
Db 160 LRGWDSREVESYPPAVGPFALYKSEFFDTVQYAVNGY-ANVRSRIGPYDY-----PT 212
QY 158 TNGS--GLALCORYHGHVDPANDTFDIDPMVVTDCIQVDPPPPPPPPSDDLTL--E 213
Db 213 PNNTMPPLKLCQNYREGTIFGFNYSYIFDPHIDEVC-----ERLPP---NVTIGVE 262
QY 214 SSSSYKNLTALKFKHLVNTIHFRLKTIINQSLINN---EIPDCYTFSLITFDNKAHSGR 270
Db 263 NYLRQRDVEVNFASLVSAQLTFKIKTVNFKA--NGGPLSAPDCFRDISITFNRRDHGQ 320
QY 271 IPISLETQAHIQECKHPSVF--QHGDNFRLLFDVVVILTCSLSLFLCARSLLRGFLIQ 327
Db 321 MLLSLDAEATRLKCHGATDFISDANFDSMLRSVLNIFVLITCALSFALCTRALWRAYLLR 380
QY 328 NEFVGFMWRQGRVISLWERLEFVNGWYILLVTSVLTISGTMKIGIEAKNLA--SYDV 385
Db 381 CTTVNFRRSQFGKLSFDGRLEFVNFYIMIFNDVLLIGSALKEQIEGRYLVVDQWDT 440
QY 386 CSILLGTSTLLVWGVIRYLTFFPHNINILIAIATLRVALPSVNRFCVAVIYLGVCFCGWI 445
Db 441 CSLFLGIGNLLVWGVIRYLTFFPHNINILIAIATLRVALPSVNRFCVAVIYLGVCFCGWL 500
QY 446 VLGPHYVKFRSLMSVSECLFSLINGDDMFVTFAMQAQQGRSSLVWLFSQLYLSFISLF 505
Db 501 ILGPYHMKFRSLATTSCLFALINGDDMFATFATLSS---KATLWFWFCQIYLYSPISLY 557


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QY      506 IYVLSLFIALITGAYDTIKHPGGAGAESELQAYI-AQCQDSPTSGKF-----RRG 556
      ||:|||||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db      558 IYVLSLFIIVMDAYDTIKAYYKDGFPITDLKAFVGTRTAEDISSGVFMTLDDDFDQTS 617
      ||:|||||:||||| ||:||||| ||:||||| ||:||||| ||:|||||

QY      557 SGSACSLLCGGR-----DPSEHS 576
      :|||||:||||| :||||| :||||| :|||||
Db      618 FLDVVKSICCCGRCGRHQEPAPQNS 642
      :|||||:||||| :||||| :||||| :|||||

```

RESULT 13
ABG01744
ID ABG01744 standard; Protein; 191 AA.
XX
AC ABG01744;

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS65931.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

PS Claim 20; SEQ ID No 32103; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Sequence	191 AA;
SQ	

Query Match 31.9%; Score 979; DB 22; Length 191;

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Best Local Similarity 98.4%; Pred. No. 3.9e-97;
Matches 183; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  MTAPAGPRGSETERLLTNPNGYGTQAGPSPAPPTPEEEDLRRRLKYFFMSPCDKFRAG 60
      |||
Db      1  MTAPAGPRGSETERELTPNPGYGTQAGPSPAPPTPEEEDLRRRLKYFFMSPCDKFRAG 60

QY     61  RKPKLMLQVVKILVVTVQLILFGLSNQLAVTPEENTIAFRHLFLLGYSDGADDTFAAY 120
      |||
Db     61  RKPKLMLQVVKILVVTVQLILFGLSNQLAVTPEENTIAFRHLFLLGYSDGADDTFAAY 120

QY    121  TREQLYQAI FHAVDQYLALPDVSLGRYAYVRGGDPWTNGSGLALCQRYYHRGHVDPAND 180
      |||
Db    121  TREQLYQAI FHAVDQYLALPDVSLGRYAYVRGGDPWTNGSGLALCQRDYHRGHVDPGND 180

QY    181  TFDIDP 186
      |||||
Db    181  TFDIDP 186

```

RESULT 14
AAU00503

ID AAU00503 standard; Protein; 193 AA.

AC AAU00503;

DT 18-JUL-2001 (first entry)

DE Human TANGO 480 protein.

Human; TANGO 315; clone jthka173a09; TANGO 330; TANGO 437; TANGO 480;
KW cellular process regulator; gene therapy; keratinocyte disorder;
KW squamous cell carcinoma; keratitis.

OS Homo sapiens.

Key	Location/Qualifiers
FH	Key
FT	Peptide
	1.19

WO200123523-A2.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 12:19:17 ; Search time 348.801 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC

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Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1101	100.0	1740	9	US-09-828-466-3
2	1101	100.0	1740	13	US-10-103-458-3
3	1101	100.0	2095	9	US-09-828-466-1
4	1101	100.0	2095	13	US-10-103-458-1
5	1100.2	99.9	2094	9	US-09-820-893-26
6	1099.4	99.9	2052	10	US-09-965-529-50
7	1099.4	99.9	2052	11	US-09-969-680A-50
8	851.4	77.3	1827	11	US-09-866-050A-608
9	851.4	77.3	1827	14	US-10-152-661-608
10	203.8	18.5	1912	11	US-09-796-753-161
11	199.8	18.1	1671	12	US-10-114-153-23
12	199.8	18.1	2067	12	US-10-114-153-27
13	199.8	18.1	2130	12	US-10-114-153-25
14	183.8	16.7	1677	12	US-10-305-810-4
15	183.8	16.7	1677	12	US-10-114-153-21
16	56	5.1	720	13	US-10-101-487-74

17	56	5.1	720	13	US-10-101-487-76	Sequence 76, Appl
18	51.8	4.7	1125	14	US-10-156-761-7230	Sequence 7230, Ap
c 19	51.8	4.7	9025608	14	US-10-156-761-1	Sequence 1, Appli
c 20	49.6	4.5	520	14	US-10-184-644-332	Sequence 332, App
c 21	49.6	4.5	520	14	US-10-184-634-332	Sequence 332, App
c 22	49.2	4.5	554	13	US-10-101-487-106	Sequence 106, App
23	49.2	4.5	783	12	US-09-953-348-99	Sequence 99, Appl
24	49.2	4.5	783	14	US-10-267-255-99	Sequence 99, Appl
25	49.2	4.5	3765	12	US-09-953-348-9	Sequence 9, Appli
26	49.2	4.5	3765	14	US-10-267-255-9	Sequence 9, Appli
c 27	49.2	4.5	53500	12	US-09-953-348-76	Sequence 76, Appl
c 28	49.2	4.5	53500	14	US-10-267-255-76	Sequence 76, Appl
29	49	4.5	2298	10	US-09-476-242-22	Sequence 22, Appl
30	49	4.5	2298	10	US-09-476-242-23	Sequence 23, Appl
31	49	4.5	2298	10	US-09-476-242-24	Sequence 24, Appl
32	49	4.5	2310	10	US-09-476-242-3	Sequence 3, Appli
33	49	4.5	2310	10	US-09-476-242-21	Sequence 21, Appl
34	49	4.5	2316	10	US-09-476-242-4	Sequence 4, Appli
35	49	4.5	2316	10	US-09-476-242-8	Sequence 8, Appli
36	49	4.5	2322	10	US-09-476-242-5	Sequence 5, Appli
37	49	4.5	2322	10	US-09-476-242-18	Sequence 18, Appl
38	49	4.5	2322	10	US-09-476-242-19	Sequence 19, Appl
39	49	4.5	2322	10	US-09-476-242-20	Sequence 20, Appl
40	49	4.5	2328	10	US-09-476-242-6	Sequence 6, Appli
41	49	4.5	2334	10	US-09-476-242-7	Sequence 7, Appli
42	49	4.5	2352	10	US-09-476-242-26	Sequence 26, Appl
43	49	4.5	2358	10	US-09-476-242-25	Sequence 25, Appl
44	49	4.5	2453	12	US-10-241-009-21	Sequence 21, Appl
45	49	4.5	2453	12	US-10-241-009-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-09-828-466-3
; Sequence 3, Application US/09828466
; Patent No. US20020035056A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
; FILE REFERENCE: MNI-125CP
; CURRENT APPLICATION NUMBER: US/09/828,466
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/544,797
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1740)
US-09-828-466-3

Query Match 100.0%; Score 1101; DB 9; Length 1740;
Best Local Similarity 100.0%; Pred. No. 1.1e-298;
Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CATTCCGGGAAGAGAACACCATCGCCTTCGACACCTCTTCTGCTGGGCTACTCGGACG	60
Db	275	CATTCCGGGAAGAGAACACCATCGCCTTCGACACCTCTTCTGCTGGGCTACTCGGACG	334
Qy	61	GAGCGGATGACACCTTCGAGCCTACACGGGGAGCAGCTGTACCGCCATCTTCCATG	120
Db	335	GAGCGGATGACACCTTCGAGCCTACACGGGGAGCAGCTGTACCGCCATCTTCCATG	394
Qy	121	CTGTGGACCACTACCTGGCGTTGCCTGACGTGTCACTGGGCCGGTATGCGTATGTCGGTG	180
Db	395	CTGTGGACCACTACCTGGCGTTGCCTGACGTGTCACTGGGCCGGTATGCGTATGTCGGTG	454

Db 1055 ATGGCTGGTACATCTCTCGTCAACGAGATGTGCTCACCATCTCGGGCACCATCAIGA 1114
QY 841 AGATCGGCATCGAGGCAAGAACTTGGCGAGCTACGAGCTCTGCGAGCATCCTCTGGGCA 900
Db 1115 AGATCGGCATCGAGGCAAGAACTTGGCGAGCTACGAGCTCTGCGAGCATCCTCTGGGCA 1174
QY 901 CCTCGACGCTGCTGGTGTGGGTGGCGTGATCCGCTACCTGACCTTCTTCCAACTACA 960
Db 1175 CCTCGACGCTGCTGGTGTGGGTGGCGTGATCCGCTACCTGACCTTCTTCCAACTACA 1234
QY 961 ATATCCTCATCGCCACACTGCGGCTGGCCCTGCCAGCGTCATGGCGCTTCTGCTGCTGG 1020
Db 1235 ATATCCTCATCGCCACACTGCGGCTGGCCCTGCCAGCGTCATGGCGCTTCTGCTGCTGG 1294
QY 1021 TGGCTGTCACTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGTGGGGCCCTATCATG 1080
Db 1295 TGGCTGTCACTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGTGGGGCCCTATCATG 1354
QY 1081 TGAAGTTCGGCTCACTCTCCA 1101
Db 1355 TGAAGTTCGGCTCACTCTCCA 1375

RESULT 3
US-09-828-466-1
; Sequence 1, Application US/09828466
; Patent No. US20020035056A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
; FILE REFERENCE: MNI-125CP
; CURRENT APPLICATION NUMBER: US/09/828,466
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/544,797
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (141)..(1880)
US-09-828-466-1

Query Match 100.0%; Score 1101; DB 9; Length 2095;
Best Local Similarity 100.0%; Pred. No. 1.2e-298;
Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATTCGGGAAGAGAAACACCATCGCCCTTCGACACCTCTTCTGCTGGGCTACTCGGACG 60
Db 415 CATTCGGGAAGAGAAACACCATCGCCCTTCGACACCTCTTCTGCTGGGCTACTCGGACG 474
QY 61 GAGCGGATGACACCTTCGCAGCCTACACGCGGGAGCAGCTGTACACGAGCCATCTTCCATG 120
Db 475 GAGCGGATGACACCTTCGCAGCCTACACGCGGGAGCAGCTGTACACGAGCCATCTTCCATG 534
QY 121 CTGTGGACCACTACCTGGCGCTTGCCTGACGTGTCACTGGGCGGGTATCGGTATGCCGTG 180
Db 535 CTGTGGACCACTACCTGGCGCTTGCCTGACGTGTCACTGGGCGGGTATCGGTATGCCGTG 594
QY 181 GTGGGGGTGACCTTGGACCAATGGCTCAGGGCTTGCTCTGCCAGCGGTACTACCAACC 240
Db 595 GTGGGGGTGACCTTGGACCAATGGCTCAGGGCTTGCTCTGCCAGCGGTACTACCAACC 654
QY 241 GAGGCCACGTGACCCCGGCCAACGACACATTTGACATTGATCCGATGGTGGTTACTGACT 300
Db 655 GAGGCCACGTGACCCCGGCCAACGACACATTTGACATTGATCCGATGGTGGTTACTGACT 714
QY 301 GCATCCAGGTGGATCCCCCGAGCGGGCCCCCTCCGCCCCCGGACGACGATCTCACCCCTCT 360

Db 715 GCATCCAGGTGGATCCCCCGAGCGGCCCTCCGCCCCCGGACGACGATCTCACCCCTCT 774
QY 361 TGGAAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAATTCACAAGCTGGTCAATGTCA 420
Db 775 TGGAAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAATTCACAAGCTGGTCAATGTCA 834
QY 421 CCATCCACTTCCGGCTGAAGACCAATTAACCTCCAGAGCCTCATCAATAATGAGATCCCGG 480
Db 835 CCATCCACTTCCGGCTGAAGACCAATTAACCTCCAGAGCCTCATCAATAATGAGATCCCGG 894
QY 481 ACTGCTATACCTTCAGCGTCTGATCACTGTTGACAAACAAGACACAGTGGCGGATCC 540
Db 895 ACTGCTATACCTTCAGCGTCTGATCACTGTTGACAAACAAGACACAGTGGCGGATCC 954
QY 541 CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGTAAAGACCCCGAGTCTTCCAGC 600
Db 955 CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGTAAAGACCCCGAGTCTTCCAGC 1014
QY 601 ACGGAGACAAACAGCTTCCGGCTCCTGTTTGACGTGGTGTGATCCTCACCTGCTCCCTGT 660
Db 1015 ACGGAGACAAACAGCTTCCGGCTCCTGTTTGACGTGGTGTGATCCTCACCTGCTCCCTGT 1074
QY 661 CCTTCTCCTCTGCGCCCGCTCACTCTTCGAGGCTTCTGCTGCAGAACGAGTTTGTGG 720
Db 1075 CCTTCTCCTCTGCGCCCGCTCACTCTTCGAGGCTTCTGCTGCAGAACGAGTTTGTGG 1134
QY 721 GGTTCATGTGGCGGCAGCGGGGACGGGTCACTCAGCCTGTGGGAGCGGCTGGAATTTGTCA 780
Db 1135 GGTTCATGTGGCGGCAGCGGGGACGGGTCACTCAGCCTGTGGGAGCGGCTGGAATTTGTCA 1194
QY 781 ATGGCTGTACATCCTGTCTGCTCACCAGCGATGTGCTCAACATCTCGGACCATCATGA 840
Db 1195 ATGGCTGTACATCCTGTCTGCTCACCAGCGATGTGCTCAACATCTCGGACCATCATGA 1254
QY 841 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCCTCCTGGGCA 900
Db 1255 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCCTCCTGGGCA 1314
QY 901 CCTCGACGCTGCTGGTGTGGTGGGCGTGATCCGCTACCTGACCTTCTTCCACAACTACA 960
Db 1315 CCTCGACGCTGCTGGTGTGGTGGGCGTGATCCGCTACCTGACCTTCTTCCACAACTACA 1374
QY 961 ATATCCTCATCGCCACACACTGCGGGTGGCGTGATCCGCTACCTGACCTTCTTCCACAACTACA 1020
Db 1375 ATATCCTCATCGCCACACACTGCGGGTGGCGTGATCCGCTACCTGACCTTCTTCCACAACTACA 1434
QY 1021 TGGCTGTACATCTACCTGGGCTACTGCTTCTGTGGTGGATCGTGTGGGCGCCCTATCATG 1080
Db 1435 TGGCTGTACATCTACCTGGGCTACTGCTTCTGTGGTGGATCGTGTGGGCGCCCTATCATG 1494
QY 1081 TGAAGTTCGGCTCACTCTCCA 1101
Db 1495 TGAAGTTCGGCTCACTCTCCA 1515

RESULT 4
US-10-103-458-1
; Sequence 1, Application US/10103458
; Publication No. US20020197680A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
; FILE REFERENCE: MNI-125
; CURRENT APPLICATION NUMBER: US/10/103,458
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US/09/544,797
; PRIOR FILING DATE: PEIOE FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2095
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (141)..(1880)
US-10-103-458-1

Query Match      100.0%; Score 1101; DB 13; Length 2095;
Best Local Similarity 100.0%; Pred. No. 1.2e-298;
Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCTCTGCTGGGCTACTCGGACG 60
Db      415 CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCTCTGCTGGGCTACTCGGACG 474

QY      61  GAGCGGATGACACCTTCGACGCTACACGCGGAGCAGCTGTACCGGCCATCTTCCATG 120
Db      475 GAGCGGATGACACCTTCGACGCTACACGCGGAGCAGCTGTACCGGCCATCTTCCATG 534

QY      121 CTGTGGACCAAGTACCTGGCGTTGCCTGACGTGTCACTGGCGCGGTATGCGTATGTCGGTG 180
Db      535 CTGTGGACCAAGTACCTGGCGTTGCCTGACGTGTCACTGGCGCGGTATGCGTATGTCGGTG 594

QY      181 GTGGGGGTGACCCCTTGACCAATGGCTCAGGCTTGCTCTCTGCGAGCGGTACTACCACC 240
Db      595 GTGGGGGTGACCCCTTGACCAATGGCTCAGGCTTGCTCTCTGCGAGCGGTACTACCACC 654

QY      241 GAGGCCACGTGGACCCGCGCCAAACGACACATTGACATTGATCCGATGGTGGTACTGACT 300
Db      655 GAGGCCACGTGGACCCGCGCCAAACGACACATTGACATTGATCCGATGGTGGTACTGACT 714

QY      301 GCATCCAGGTGGATCCCCCGAGCGGCCCTCCGCCCCCGAGCGACGATCTCACCCCTCT 360
Db      715 GCATCCAGGTGGATCCCCCGAGCGGCCCTCCGCCCCCGAGCGACGATCTCACCCCTCT 774

QY      361 TGGAAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAATTCACAGCTGGTCAATGTCA 420
Db      775 TGGAAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAATTCACAGCTGGTCAATGTCA 834

QY      421 CCATCCACTTCGGGTGAAGACCATTAACCTCCAGAGCCTCATCAATAATGAGATCCCCG 480
Db      835 CCATCCACTTCGGGTGAAGACCATTAACCTCCAGAGCCTCATCAATAATGAGATCCCCG 894

QY      481 ACTGCTATACCTTCAGGTCCTGTATCAGCTTGACAAACAAAGCACACAGTGGCGGATCC 540
Db      895 ACTGCTATACCTTCAGGTCCTGTATCAGCTTGACAAACAAAGCACACAGTGGCGGATCC 954

QY      541 CCATCAGCCTGGAGACCCAGGCCCAATCCAGGAGTGTAAAGCAACCCAGTGTCTTCCAGC 600
Db      955 CCATCAGCCTGGAGACCCAGGCCCAATCCAGGAGTGTAAAGCAACCCAGTGTCTTCCAGC 1014

QY      601 ACGGAGACAAACAGCTTCGGGTCCTGTGTTGACGTGGTGTATCTCATCTCACCTGCTCCCTGT 660
Db      1015 ACGGAGACAAACAGCTTCGGGTCCTGTGTTGACGTGGTGTATCTCATCTCACCTGCTCCCTGT 1074

QY      661 CCTTCTCTCTGCGCCCGCTCACTCCTTCGAGGCTTCCTGCTGAGAACGAGTTTGTG 720
Db      1075 CCTTCTCTCTGCGCCCGCTCACTCCTTCGAGGCTTCCTGCTGAGAACGAGTTTGTG 1134

QY      721 GGTTCATGTGGGCGAGCGGGGACCGGTTCATCAGCCTGTGGGAGCGGTGGAATTTGTCA 780
Db      1135 GGTTCATGTGGGCGAGCGGGGACCGGTTCATCAGCCTGTGGGAGCGGTGGAATTTGTCA 1194

QY      781 ATGGCTGGTACATCTCTGCTCGTCACCGAGATGTGCTCACCATCTCGGGCACCATCATGA 840
Db      1195 ATGGCTGGTACATCTCTGCTCGTCACCGAGATGTGCTCACCATCTCGGGCACCATCATGA 1254

QY      841 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGAGCTGTGAGCATCTCTCTGGGCA 900
Db      1255 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGAGCTGTGAGCATCTCTCTGGGCA 1314

QY      901 CCTCGACGCTGCTGGTGTGGGTGGCGGTGATCCGCTACCTGACCTTCTTCCACAATACA 960
Db      1315 CCTCGACGCTGCTGGTGTGGGTGGCGGTGATCCGCTACCTGACCTTCTTCCACAATACA 1374
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QY      961 ATATCTCTCATCGCCACACTCGGGTGGCCCTGCCAGCGTCATCGCTTCTGCTGCTGCG 1020
Db      1375 ATATCTCTCATCGCCACACTCGGGTGGCCCTGCCAGCGTCATCGCTTCTGCTGCTGCG 1434

QY      1021 TGGCTGTCTATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTCTGGGGCCCTATCATG 1080
Db      1435 TGGCTGTCTATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTCTGGGGCCCTATCATG 1494

QY      1081 TGAAGTTCCGCTCACTCTCCA 1101
Db      1495 TGAAGTTCCGCTCACTCTCCA 1515

RESULT 5
US-09-820-893-26
; Sequence 26, Application US/09820893
; Patent No. US20020076705A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 31 Human Secreted Proteins
; FILE REFERENCE: P2033P1
; CURRENT APPLICATION NUMBER: US/09/820,893
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/531,119
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/102,895
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2094
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2078)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-820-893-26
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Query Match      99.9%; Score 1100.2; DB 9; Length 2094;
Best Local Similarity 99.8%; Pred. No. 2e-298;
Matches 1099; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1  CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCTGCTGGGCTACTCGGACG 60
Db      382 CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCTGCTGGGCTACTCGGACG 441

QY      61  GAGCGGATGACACCTTCGACGCTACACGCGGAGCAGCTGTACAGGCCATCTTCCATG 120
Db      442 GAGCGGATGACACCTTCGACGCTACACGCGGAGCAGCTGTACAGGCCATCTTCCATG 501

QY      121 CTGTGGACCAAGTACCTGGCGTTGCCTGACGTGTCACTGGGCGGATGCGGTATGTCGGTG 180
Db      502 CTGTGGACCAAGTACCTGGCGTTGCCTGACGTGTCACTGGGCGGATGCGGTATGTCGGTG 561

QY      181 GTGGGGGTGACCCCTTGGACCAATGGCTCAGGGCTTGTCTCTGCCAGCGGTACTACCACC 240
Db      562 GTGGGGGTGACCCCTTGGACCAATGGCTCAGGGCTTGTCTCTGCCAGCGGTACTACCACC 621

QY      241 GAGGCCACGTGGACCCCGGCCAACGACACATTTGACATTTGATCCGATGGTGGTACTGACT 300
Db      622 GAGGCCACGTGGACCCCGGCCAACGACACATTTGACATTTGATCCGATGGTGGTACTGACT 681

QY      301 GCATCCAGGTGGATCCCCCGAGCGGCCCTCCGCCCCCGAGCGACGATCTCACCCCTCT 360
Db      682 GCATCCAGGTGGATCCCCCGAGCGGCCCTCCGCCCCCGAGCGACGATCTCACCCCTCT 741

QY      361 TGGAAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAATTCACAAAGCTGGTCAATGTCA 420
Db      742 TGGAAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAATTCACAAAGCTGGTCAATGTCA 801

QY      421 CCATCCACTTCGGGTGAAGACCATTAACCTCCAGAGCCTCATCAATAATGAGATCCCCG 480
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Db 802 CCATCCACTTCGGCTGAAGACCATTAACCTCCAGAGCCTCATCAATAATGAGATCCCGG 861
Qy 481 ACTGCTATACCTTCAGCGTCTGTGATCACGTTTGACAAAGACACACAGTGGCGGATCC 540
Db 862 ACTGCTATACCTTCAGCGTCTGTGATCACGTTTGACAAAGACACACAGTGGCGGATCC 921
Qy 541 CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGAAGACACCCAGTGTCTCCAGC 600
Db 922 CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGAAGACACCCAGTGTCTCCAGC 981
Qy 601 ACGGAGACAAACAGCTTCGGGCTCCTGTTTGACGTTGGTGGTCACTCCTCACCTTGCTCCCTGT 660
Db 982 ACGGAGACAAACAGCTTCGGGCTCCTGTTTGACGTTGGTGGTCACTCCTCACCTTGCTCCCTGT 1041
Qy 661 CTTTCTCTCTCTGCGCCCGCTCACTCCTTCGAGGCTTCCTGCTGCAGAACGAGTTTGTGG 720
Db 1042 CTTTCTCTCTCTGCGCCCGCTCACTCCTTCGAGGCTTCCTGCTGCAGAAAGAGTTTGTGG 1101
Qy 721 GGTTCATGTGGCGGACCGGGACCGGTCATCAGCCTGTGGGAGCGGCTGGAATTTGTCA 780
Db 1102 GGTTCATGTGGCGGACCGGGACCGGTCATCAGCCTGTGGGAGCGGCTGGAATTTGTCA 1161
Qy 781 ATGGCTGTACATCCTGTCTGCTACCCAGCGGTCACTCAGCGATGTGCTACCATCTCGGGACCATCATGA 840
Db 1162 ATGGCTGTACATCCTGTCTGCTACCCAGCGGTCACTCAGCGATGTGCTACCATCTCGGGACCATCATGA 1221
Qy 841 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCTCCTCGGGCA 900
Db 1222 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCTCCTCGGGCA 1281
Qy 901 CCTCGACGCTGCTGTTGGTGGGCGTGTATCCGCTACCTGACCTTCTTCCACAACATA 960
Db 1282 CCTCGACGCTGCTGTTGGTGGGCGTGTATCCGCTACCTGACCTTCTTCCACAACATA 1341
Qy 961 ATATCCTCATCGCCACACTGCGGGTGGCCCTGCCAGCGTCACTGCGCTTCTGCTGCTGG 1020
Db 1342 ATATCCTCATCGCCACACTGCGGGTGGCCCTGCCAGCGTCACTGCGCTTCTGCTGCTGG 1401
Qy 1021 TGGCTGTATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGTGGGCGCCTATCATG 1080
Db 1402 TGGCTGTATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGTGGGCGCCTATCATG 1461
Qy 1081 TGAAGTTCGGCTCACTCTCCA 1101
Db 1462 TGAAGTTCGGCTCACTCTCCA 1482
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RESULT 6

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US-09-965-529-50
; Sequence 50, Application US/09965529
; Publication No. US20020182671A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731 USA
; CURRENT APPLICATION NUMBER: US/09/965,529
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 50
; LENGTH: 2052
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 977658CB1
US-09-965-529-50
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Query Match 99.9%; Score 1099.4; DB 10; Length 2052;
Best Local Similarity 99.9%; Pred. No. 3.4e-298;
Matches 1100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 CATTCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCTGCTGGGCTACTCGGACG 60
Db 382 CATTCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCTGCTGGGCTACTCGGACG 441
Qy 61 GACGGGATGACACCTTCGCGAGCCTACACGGGAGAGAGCTGTACCCAGGCCATCTTCCATG 120
Db 442 GACGGGATGACACCTTCGCGAGCCTACACGGGAGAGAGCTGTACCCAGGCCATCTTCCATG 501
Qy 121 CTGTGGACCAGTACCTTGGCGGTTGCCCTGACGTGTCACTGGGCCGGTATGCGTATGCCGTG 180
Db 502 CTGTGGACCAGTACCTTGGCGGTTGCCCTGACGTGTCACTGGGCCGGTATGCGTATGCCGTG 561
Qy 181 GTGGGGGTGACCCCTTGGACCAATGGCTCAGGGCTTGTCTCTGTGCCAGCGGTACTACCACC 240
Db 562 GTGGGGGTGACCCCTTGGACCAATGGCTCAGGGCTTGTCTCTGTGCCAGCGGTACTACCACC 621
Qy 241 GAGGCCACGTGGACCCGGCCAAACGACACATTTGACATTTGATCCGATGGTGGTACTGACT 300
Db 622 GAGGCCACGTGGACCCGGCCAAACGACACATTTGACATTTGATCCGATGGTGGTACTGACT 681
Qy 301 GCATCCAGTGGATCCCCCGAGCGGCCCTCCGCCCGCCAGCGACGATCTCACCCCTCT 360
Db 682 GCATCCAGTGGATCCCCCGAGCGGCCCTCCGCCCGCCAGCGACGATCTCACCCCTCT 741
Qy 361 TGGAAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAATTTCCACAAGCTGGTCAATGTCA 420
Db 742 TGGAAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAATTTCCACAAGCTGGTCAATGTCA 801
Qy 421 CCATCCACTTCCGGCTGAAGACCATTAACCTCCAGAGCCTCATCAATAATGAGATCCCGG 480
Db 802 CCATCCACTTCCGGCTGAAGACCATTAACCTCCAGAGCCTCATCAATAATGAGATCCCGG 861
Qy 481 ACTGCTATACCTTCAGCGTCTGTATCACGTTTGACAAACAAAGACACAGTGGCGGATCC 540
Db 862 ACTGCTATACCTTCAGCGTCTGTATCACGTTTGACAAACAAAGACACAGTGGCGGATCC 921
Qy 541 CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGAAGACACCCAGTGTCTTCCAGC 600
Db 922 CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGAAGACACCCAGTGTCTTCCAGC 981
Qy 601 ACGGAGACAAACAGCTTCGGGCTCCTGTTTGACGTTGGTGGTCACTCCTCACCTGCTCCCTGT 660
Db 982 ACGGAGACAAACAGTTTCGGGCTCCTGTTTGACGTTGGTGGTCACTCCTGCTCCCTGT 1041
Qy 661 CTTTCTCTCTCTGCGCCCGCTCACTCCTTCGAGGCTTCCTGCTGCAGAACGAGTTTGTGG 720
Db 1042 CTTTCTCTCTCTGCGCCCGCTCACTCCTTCGAGGCTTCCTGCTGCAGAAAGAGTTTGTGG 1101
Qy 721 GGTTCATGTGGCGGACCGGGACCGGTCATCAGCCTGTGGGAGCGGCTGGAATTTGTCA 780
Db 1102 GGTTCATGTGGCGGACCGGGACCGGTCATCAGCCTGTGGGAGCGGCTGGAATTTGTCA 1161
Qy 781 ATGGCTGTATCATCCTGTCTGCTACCCAGCGGTGTGCTCACCATCTCGGGACCATCATGA 840
Db 1162 ATGGCTGTATCATCCTGTCTGCTACCCAGCGGTGTGCTCACCATCTCGGGACCATCATGA 1221
Qy 841 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGCTGTGAGCATCTCCTCGGGCA 900
Db 1222 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGCTGTGAGCATCTCCTCGGGCA 1281
Qy 901 CCTCGACGCTGCTGTTGGTGGGCGTGTATCCGCTACCTGACCTTCTTCCACAACATA 960
Db 1282 CCTCGACGCTGCTGTTGGTGGGCGTGTATCCGCTACCTGACCTTCTTCCACAACATA 1341
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QY 961 ATATCCTCATCGCCACACTGGGGTGGCCCTGCCAGCGTATGCGCTTCTGCTGCTGCG 1020
Db 1342 ATATCCTCATCGCCACACTGGGGTGGCCCTGCCAGCGTATGCGCTTCTGCTGCTGCG 1401
QY 1021 TGGCTGTATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGGTGGGCGCCCTATCATG 1080
Db 1402 TGGCTGTATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGGTGGGCGCCCTATCATG 1461
QY 1081 TGAAGTTCGGCTCACTCTCCA 1101
Db 1462 TGAAGTTCGGCTCACTCTCCA 1482

RESULT 7
US-09-969-680A-50
; Sequence 50, Application US/09969680A
; Publication No. US20030124649A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti; YUE, Henry
; APPLICANT: TANG, Y. Tom; BANDMAN, Olga
; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731-1 USA
; CURRENT APPLICATION NUMBER: US/09/969,680A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US00/22315
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/149,641
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/164,203
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 50
; LENGTH: 2052
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124649A1 977658CB1
US-09-969-680A-50

Query Match 99.9%; Score 1099.4; DB 11; Length 2052;
Best Local Similarity 99.9%; Pred No. 3.4e-298;
Matches 1100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTCCTGCTGGGCTACTCGGACG 60
Db 382 CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTCCTGCTGGGCTACTCGGACG 441
QY 61 GAGCGATGACACCTTCGAGCCTACACGCGGAGCAGCTGTACCGCCATCTTCCATG 120
Db 442 GAGCGATGACACCTTCGAGCCTACACGCGGAGCAGCTGTACCGCCATCTTCCATG 501
QY 121 CTGTGGACCAAGTACCTGGCGTTCCTGACGTGTCACTGGGCGGTATGCGTATGTCGGTG 180
Db 502 CTGTGGACCAAGTACCTGGCGTTCCTGACGTGTCACTGGGCGGTATGCGTATGTCGGTG 561
QY 181 GTGGGGTGACCCCTTGGACCAATGGCTCAGGGCTTGTCTCTGCCAGCGGTACTACCACC 240
Db 562 GTGGGGTGACCCCTTGGACCAATGGCTCAGGGCTTGTCTCTGCCAGCGGTACTACCACC 621
QY 241 GAGGCCAGTGGACCCCGGCCAACGACACATTTGACATTGATCCGATGGTGGTACTGACT 300
Db 622 GAGGCCAGTGGACCCCGGCCAACGACACATTTGACATTGATCCGATGGTGGTACTGACT 681
QY 301 GCATCCAGGTGGATCCCCCGAGCGGCCCTCCGCGCCCGCCAGCGACGATCTCACCTCT 360
Db 682 GCATCCAGGTGGATCCCCCGAGCGGCCCTCCGCGCCCGCCAGCGACGATCTCACCTCT 741

QY 361 TGGAAAGCAGCTCCAGTTACAGAACCTCAGCTCAAAATTCACAAGCTGGTCAATGTCA 420
Db 742 TGGAAAGCAGCTCCAGTTACAGAACCTCAGCTCAAAATTCACAAGCTGGTCAATGTCA 801
QY 421 CCATCCACTTCCGGCTGAAGACCATTAACCTCCAGAGCCTCATCAATAATGATCCCCGG 480
Db 802 CCATCCACTTCCGGCTGAAGACCATTAACCTCCAGAGCCTCATCAATAATGATCCCCGG 861
QY 481 ACTGTATACCTTCCAGCTCCTGATCACGTTTGTGACAAACAAAGCACACAGTGGGCGGATCC 540
Db 862 ACTGTATACCTTCCAGCTCCTGATCACGTTTGTGACAAACAAAGCACACAGTGGGCGGATCC 921
QY 541 CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGAAGCACCCAGTGTCTTCCAGC 600
Db 922 CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGAAGCACCCAGTGTCTTCCAGC 981
QY 601 ACGGAGACAAACAGCTTCCGCTCCTGTTTGACGTTGGTGGTCACTCCTCACCTGCTCCCTGT 660
Db 982 ACGGAGACAAACAGCTTCCGCTCCTGTTTGACGTTGGTGGTCACTCCTCACCTGCTCCCTGT 1041
QY 661 CCTTCTCCTCTCGGCCGCTCACTCCTTCGAGGTTTCCGTGTCAGAACAGTGTGG 720
Db 1042 CCTTCTCCTCTCGGCCGCTCACTCCTTCGAGGTTTCCGTGTCAGAACAGTGTGG 1101
QY 721 GGTTCATGTGGCGGACGCGGACGGGTCACTAGCCTGTGGAGCGGCTGGAATTTGTCA 780
Db 1102 GGTTCATGTGGCGGACGCGGACGGGTCACTAGCCTGTGGAGCGGCTGGAATTTGTCA 1161
QY 781 ATGGCTGGTACATCCTGCTCGTCACAGCGATGTCACCATCTCGGGACCATCATGA 840
Db 1162 ATGGCTGGTACATCCTGCTCGTCACAGCGATGTCACCATCTCGGGACCATCATGA 1221
QY 841 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCCTCCTGGGCA 900
Db 1222 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCCTCCTGGGCA 1281
QY 901 CCTCGACGCTGCTGTGGTGGGCGTGTATCGGCTACCTGACCTTCTTCCACAACATA 960
Db 1282 CCTCGACGCTGCTGTGGTGGGCGTGTATCGGCTACCTGACCTTCTTCCACAACATA 1341
QY 961 ATATCCTCATCGCCACACTGCGGGTGGCCCTGCCAGCGTCACTGCTGCTGCTGCG 1020
Db 1342 ATATCCTCATCGCCACACTGCGGGTGGCCCTGCCAGCGTCACTGCTGCTGCTGCG 1401
QY 1021 TGGCTGTATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGGGCGCCCTATCATG 1080
Db 1402 TGGCTGTATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGGGCGCCCTATCATG 1461
QY 1081 TGAAGTTCGGCTCACTCTCCA 1101
Db 1462 TGAAGTTCGGCTCACTCTCCA 1482

RESULT 8
US-09-866-050A-608
; Sequence 608, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c4U
; CURRENT APPLICATION NUMBER: US/09/866,050A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 608
; LENGTH: 1827

i	TYPE: DNA	Query Match	77.3%;	Score 851.4;	DB 11;	Length 1827;
;	ORGANISM: Mouse	Best Local Similarity	85.8%;	Pred. No. 1.2e-228;		
US-09-866-050A-608		Matches 945;	Conservative 0;	Mismatches 156;	Indels 0;	Gaps 0;
Qy	1	CATTCCGGGAAGACAAACACCATCGCCTTCCGACACTCTTCTCTGCTGGGCTACTCGGACG	60			
Db	167	CATTCCGGGAAGAGAAACACCAATTGCCTTCCGACATCTCTTCTCTGCTGGGTTACTCTGATG	226			
Qy	61	GAGCGGATGACACTTTCGAGCCTACACGGGGAGCAGCTGTACCAGGCCATCTTCCATG	120			
Db	227	GGTCTGATGACACCTTTCGAGCCTACACACAGGAGCAGCTCTACCAAGCCATCTTCTATG	286			
Qy	121	CTGTGGACCACTTTCGCGGTTGCCTGACGTGTACTGGGCCGGTATGCGTATGTCGGTG	180			
Db	287	CTGTGGACCACTTTCGCGGTTGCCTGACGTGTACTGGGCCGGTATGCGTATGTCGGTG	346			
Qy	181	GTGGGGGTGACCCCTTGGACCAATGGCTCAGGGCTTGGTCTCTGCCAGCGGTACTACCACC	240			
Db	347	GTGGGGGTGGGCTTGGGCCAATGGATCAGCTTTGGCTCTCTGCCAGCGGTACTACCACC	406			
Qy	241	GAGGCCACGTGGACCCGGCCCAACGACACATTTGACATTGATCCGATGGTGGTTACTGACT	300			
Db	407	GTGGCCATGTGGACCCAGCCCAATGATACCTTTGACATTGATCCAAAGGTAGTCACTGACT	466			
Qy	301	GCATCCAGGTGGATCCCCCGAGCGGCCCTTCCGCCCCCAGCGACGATCTCACCTCT	360			
Db	467	GTATCCAGGTGGATCCCCCGAGCGGCCCTTCCGCCCCCAGCGACGATCTCACCTCT	526			
Qy	361	TGAAAGCAGCTCCAGTTACAAGAACCTCAAGCTCAAATTCACAAGCTGGTCAATGTCA	420			
Db	527	TGGATGGCAGCCAGTTACAAGAACCTCAACACTGAAATTCACAAGCTGATCAACGTCA	586			
Qy	421	CCATCCACTTCCGGCTGAAGACCATTAACCTCCAGACCTCATCAATAATGAGATCCCGG	480			
Db	587	CCATCCACTTCCAGCTGAAGACCAATTAACCTGCAGACCTCATCAACAATGAGATCCCGT	646			
Qy	481	ACTGCTATACCTTCAGCGTCTGTATCACGTTTGACAACAAAAGCACACAGTGGCGGATCC	540			
Db	647	ATTGTTACACCTTCAGTATCCTGATCACATTTGACAATAAAGGCGCACAGTGGCGGATCC	706			
Qy	541	CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGTAAAGCACCCAGTGTCTTCCAGC	600			
Db	707	CCATCCGCCCTGGAGACCAAGACCCACATCCAGGAGTGTAAACACACCCAGTGTCTCCAGAC	766			
Qy	601	ACGGAGACAACAGCTTCCGGCTCCTGTTTGACGTGGTGGTTCATCCTCACCTGCTCCCTGT	660			
Db	767	ATGGAGACAACAGCTTCCGGCTCCTGTTTGATGTGGTGGTTATCCTCACCTGCTCCCTGT	826			
Qy	661	CCTTCCTCTCTGCGCCCGCTCACTCCTTCGAGGCTTCTGTGCAGAACGAGTTGTGG	720			
Db	827	CCTTCCTCTCTGCGCCCGCTCACTGCTCCGTGGCTTCTGTGCAGAACGAGTTGTGG	886			
Qy	721	GGTTCATGTGGCGGCAGCGGGACGGGTTCATCAGCCTGTGGAGCGGCTGGAATTTGTCA	780			
Db	887	TATTCATGTGGCGGCAGCGGGTTCGGGAAATCAGCCTCTGGGAACGGCTGGAGTTGTCA	946			
Qy	781	ATGGCTGGTACATCCTGTCTGTCACCAAGCATGTGCTCACCATCTCGGGCACCATCATGA	840			
Db	947	ATGGCTGGTACATCCTGTCTGTCACCAAGCATGTGCTCACCATCTCGGGCACCATCATGA	1006			
Qy	841	AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCTCCTCGGGCA	900			
Db	1007	AGATTGGCATTTGAGGCAAGAAACCTAGCCAGCTATGATGTCTGCAGTATTTCTCTGGGTA	1066			
Qy	901	CCTCGACGCTGCTGTGTGGGTGGCGGTGATCCGCTACCTGACCTTCTTCCACAACACTACA	960			
Db	1067	CCTCCACTCTGTAGTCTGGGTGGGTGATCTGCTACCTGACATTTTCCACAAGTACA	1126			
Qy	961	ATATCTCATGCCACACTGCGGGTGGCCCTGCCAGCGTTCATGCGTTCTGTGCTGCGG	1020			

Db	1127	ACATCTTGATTGCCACGTTGCGAGTGGCACTGCCAGTGTCTGCTGCTGTG	1186
QY	1021	TGGCTGTCACTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGTGGGGCCCTATCATG	1080
Db	1187	TGGCTGTCACTACCTGGGCTATTGCTTCTGTGGCTGGATCGTGTAGGGCCCTACCATG	1246
QY	1081	TGAAGTTCGGCTCACTCTCCA	1101
Db	1247	TGAAGTTCGGCTCGCTGTCCA	1267

RESULT 9
 US-10-152-661-608
 ; Sequence 608, Application US/10152661
 ; Publication No. US20030022835A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Strachan, Lorna
 ; APPLICANT: Sleeman, Matthew
 ; APPLICANT: Onrust, Rene
 ; APPLICANT: Murison, James G.
 ; APPLICANT: Kumble, Krishanand D.
 ; TITLE OF INVENTION: Compositions Isolated From Skin Cells
 ; TITLE OF INVENTION: and Methods for Their Use
 ; FILE REFERENCE: 11000.1011c5
 ; CURRENT APPLICATION NUMBER: US/10/152,661
 ; CURRENT FILING DATE: 2002-05-20
 ; PRIOR APPLICATION NUMBER: 09/866,050
 ; PRIOR FILING DATE: 2001-05-24
 ; PRIOR APPLICATION NUMBER: 60/221,232
 ; PRIOR FILING DATE: 2000-07-25
 ; PRIOR APPLICATION NUMBER: 60/206,650
 ; PRIOR FILING DATE: 2000-05-24
 ; PRIOR APPLICATION NUMBER: 09/312,283
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: PCT/NZ99/00051
 ; PRIOR FILING DATE: 1999-04-29
 ; PRIOR APPLICATION NUMBER: 09/188,930
 ; PRIOR FILING DATE: 1998-11-09
 ; PRIOR APPLICATION NUMBER: 09/069,726
 ; PRIOR FILING DATE: 1998-04-29
 ; NUMBER OF SEQ ID NOS: 725
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 608
 ; LENGTH: 1827
 ; TYPE: DNA
 ; ORGANISM: Mouse
 US-10-152-661-608

Query Match	77.3%;	Score	851.4;	DB	14;	Length	1827;
Best Local Similarity	85.8%;	Pred. No.	1.2e-228;				
Matches	945;	Conservative	0;	Mismatches	156;	Indels	0;
QY	1	CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCCCTGCTGGGTACTCGGACG	60				
Db	167	CATTCCGGGAAGAGAACACCATTTGCCTTCCGACATCTCTTCCCTGCTGGGTACTCTGATG	226				
QY	61	GAGCGGATGACACCTTCGCAGCCTACACGGGGAGCAGCTGTACCAGGCCATCTTCCATG	120				
Db	227	GGTCTGATGACACCTTTGCAGCCTACACAGGAGCAGCTCTACCAAGCCATCTTCTATG	286				
QY	121	CTGTGGACCAGTACCTTGGCGTTTGCCTGACGTGTCACTGGGCGGGTATGCGTATGTCGGTG	180				
Db	287	CTGTGGACCAGTACCTGTATACCTGAGATATCCCTGGGCGGGTATGCCCTATGTCGGTG	346				
QY	181	GTGGGGGTGACCCCTTGGACCAATGGCTCAGGGCTTGCTCTCTGCCAGCGGTACTACCACC	240				
Db	347	GTGGGGGTGGCCCTTGGGCCAATGGATCAGCTTTGGCTCTCTGCCAGCGGTACTACCACC	406				
QY	241	GAGGCACGTGGACCCGGCCAAACGACACATTTGACATTGATCCGATGGTGGTTACTGACT	300				
Db	407	GTGGCCATGTGGACCCAGCCCAATGATACCTTTGACATTGATTCGAAGGGTAGTCACTGACT	466				

Sequence 27, Application US/10114153
Publication No. US20030185815A1
GENERAL INFORMATION:
APPLICANT: Padigar, Muralidhara
APPLICANT: Shenoy, Suresh
APPLICANT: Kekuda, Ramesh
APPLICANT: Rastelli, Luca
APPLICANT: Mezes, Peter
APPLICANT: Smithson, Glennda
APPLICANT: Guo, Xiaojia
APPLICANT: Gerlach, Valerie
APPLICANT: Casman, Stacie
APPLICANT: Boldog, Ferenc
APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan
APPLICANT: Tchernev, Velizar
APPLICANT: Gangolli, Esha
APPLICANT: Vernet, Corine
APPLICANT: Spytek, Kimberly
APPLICANT: Malyankar, Uriel
APPLICANT: Patturajan, Meera
APPLICANT: Miller, Charles
APPLICANT: Taupier, Raymond J. Jr.
APPLICANT: Heyes, Melvyn
APPLICANT: Ju, Jingfang
APPLICANT: Peyman, John
APPLICANT: Catterton, Elina
APPLICANT: MacDougall, John
APPLICANT: Edinger, Shlomit
APPLICANT: Stone, David
APPLICANT: Mazur, Ann
TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACID
TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
FILE REFERENCE: 21402-322A
CURRENT APPLICATION NUMBER: US/10/114,153
CURRENT FILING DATE: 2002-08-06
PRIOR APPLICATION NUMBER: 60/281086
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281906
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282020
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282930
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283512
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/283444
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/283657
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283710
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283678
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284234
PRIOR FILING DATE: 2001-04-17
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 251
SEQ ID NO 27
LENGTH: 2067
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (93)..(1791)
US-10-114-153-27

Query Match 18.1%; Score 199.8; DB 12; Length 2067;
Best Local Similarity 56.2%; Pred. No. 6.9e-46;
Matches 398; Conservative 0; Mismatches 304; Indels 6; Gaps 1;
386 CCTCAGCTCAAAATTCACAGCTGGTCAATGTCCACCATCCACCTCCGGCTGAAGACCAT 445

Db 722 CTTCAGACTGGAATTTTATCGGCTCTTACAGGTTGAAATCTCCTTTTCATCTTAAAGGCAT 781
Qy 446 TAACCTCCAGAGCCTCATCAATAATAGATCCCGACTGCTATACCTTACAGCTCCTGAT 505
Db 782 TGACCTACAGACAATTCAATCCCGTGAGTTACAGACTGTTATGCTTTTTCAGAAATACGAT 841
Qy 506 CACGTTTGGACAAAGACACACAGTGGGGGATCCCCATCAGCTGGAGACCCAGGCCA 565
Db 842 TATCTTTGACATAAAGCTCACAGTGGCAAAATCAAAATCTATTTGACAGTATGCCAA 901
Qy 566 CATCCAGGAGTGAAGCACCCAGTCTTCCAGCAGGAGACAAACAGCTTCCGG----- 620
Db 902 AATTGAAGATGTAAGACTTGAACATATTGGATCAGCTCAGAAAATGCTCAGTATGT 961
Qy 621 -CTCCTGTTTGACGTGGTGGTCACTCCTCACCTGCTCCCTGCTCCTTCTCCTCGGCCCG 679
Db 962 CCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1021
Qy 680 CTCACCTCCTTCGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 739
Db 1022 ATCCATTGTTCTTCTCTAAGTTACGGAAGAGATTTCTAAATTTCTTCTCGGAGAGTA 1081
Qy 740 GGGACGGGTCAATCAGCCTGTGGAGCGGCTGGAATTTGTCAATGGTGGTGGTGGTGGTGGT 799
Db 1082 CAAGCGGCTGCTGTGTGACACCGACAGTGGGAGTTTCATCAACGGCTGGTATGCTCCTGGT 1141
Qy 800 CGTCACCGAGGATGTGCTCACCATCTCGGGCACCATCATGAAGATCGGACCGGCCAA 859
Db 1142 GATTATCAGGACCTAATGACAATCATGCTGGCTCCATATTAATAATGGAATCAAAGCAA 1201
Qy 860 GAACTTGGGAGCTACGACGTCTGACGATCCTCCTGGGCACCTCGACGCTGCTGGTGGT 919
Db 1202 GAATCTCACAACATATGATCTCTGACGATTTTCTTGGAACTCTACGCTCTTGGTTG 1261
Qy 920 GGTGGCGGTGATCCGCTACCTGACCTTCTTCCACAACACTACAATATCCTCATCGCCACACT 979
Db 1262 GGTGGAGTCAATCAGATACCTGGGTATTTCCAGGCATATAATGTAATGTAATGTAATGTA 1321
Qy 980 GCGGGTGGCCCTGCCCCAGCGTCAATGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1039
Db 1322 GCAGGCCTCACTGCCAAAAGTTCTTCGGTTTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 1381
Qy 1040 CTACTGCTTCTGCTGGTGGATCGTGGTGGGCTTATCATATGTAAGTT 1087
Db 1382 TTACACATTCTGCTGGCTGGAATGCTTAGGACCATACCATGACAAGTT 1429

RESULT 13
US-10-114-153-25
Sequence 25, Application US/10114153
Publication No. US20030185815A1
GENERAL INFORMATION:
APPLICANT: Padigar, Muralidhara
APPLICANT: Shenoy, Suresh
APPLICANT: Kekuda, Ramesh
APPLICANT: Rastelli, Luca
APPLICANT: Mezes, Peter
APPLICANT: Smithson, Glennda
APPLICANT: Guo, Xiaojia
APPLICANT: Gerlach, Valerie
APPLICANT: Casman, Stacie
APPLICANT: Boldog, Ferenc
APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan
APPLICANT: Tchernev, Velizar
APPLICANT: Gangolli, Esha
APPLICANT: Vernet, Corine
APPLICANT: Spytek, Kimberly
APPLICANT: Malyankar, Uriel
APPLICANT: Patturajan, Meera
APPLICANT: Miller, Charles
APPLICANT: Taupier, Raymond J. Jr.
APPLICANT: Heyes, Melvyn

APPLICANT: Ju, Jingfang
APPLICANT: Peyman, John
APPLICANT: Catterton, Elina
APPLICANT: MacDougall, John
APPLICANT: Edinger, Shlomit
APPLICANT: Stone, David
APPLICANT: Mazur, Ann
TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACID
TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
FILE REFERENCE: 21402-322A
CURRENT APPLICATION NUMBER: US/10/114,153
CURRENT FILING DATE: 2002-08-06
PRIOR APPLICATION NUMBER: 60/281086
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281906
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282020
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282930
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283512
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/283444
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/283657
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283710
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283678
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284234
PRIOR FILING DATE: 2001-04-17
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 251
SEQ ID NO 25
LENGTH: 2130
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (31)..(1645)
US-10-114-153-25

Query Match 18.1%; Score 199.8; DB 12; Length 2130;
Best Local Similarity 56.2%; Pred. No. 7e-46;
Matches 398; Conservative 0; Mismatches 304; Indels 6; Gaps 1;
QY 386 CCTCAGCTCAAAATCCACAAGCTGGTCAATGTCACCATCCACTTCCGGCTGAAGACCAT 445
Db 576 CTTCAGACTGGAATTTATCGGCTCTTACAGTTGAAATCTCCCTTCATCTTAAAGGCAT 635
QY 446 TAACCTCCAGAGCCCTCATCAATAATGAGATCCCGGACTGCTATACCTTCAGGTCCTGAT 505
Db 636 TGACCTACAGACAATTCATTCCCGTGAGTTACAGACTGTTATGTTTTCAGAAATACGAT 695
QY 506 CACGTTTGACAACAAAGCACACAGTGGGGGATCCCATCAGCCAGGAGACACAGCTTCCGG 505
Db 696 TATCTTTGACAATAAAGCTCACAGTGGCAAAATCAAAATCTATTTTGACAGTATGCCAA 755
QY 566 CATCCAGGAGTGAAGCACCCAGTGTCTTCCAGCACGGAGACACAGCTTCCGG----- 620
Db 756 AATTGAAGAATGTAAAGACTTGAACATATTTGGATCAGCTCAGTCAAGAAATGCTCAGTATGT 815
QY 621 -CTCCTGTTTGACGTGGTGGTTCATCCTCAGCTGCTCCCTGCTCCTTCTCCTCTGCGCCCG 679
Db 816 CTTGGTGTGATGCAATTTGTCATTGTTGATTTGCTTGGCATCTCTATTTCTGTGTACAG 875
QY 680 CTCACCTCTCGAGGTTCTCTGCTGCAGAACAGTTTGTGGGTTTCATGTGGCGGACGCG 739
Db 876 ATCCATTGTTCTTGTCTAAGTTACGGAAGAGATTTCTAAATTTCTCTCTGGAGAAGTA 935
QY 740 GGGACGGGTCAATCAGCTGTGGGAGCGGTGGAATTTGTCAATGGCTGGTACATCCTGCT 799

Db 936 CAAGCGGCCTGTGTGTGACACCGACCGAGTTCATCAACGGCTGGTATGTCTCTGGT 995
QY 800 CGTCACCAGCGATGTGCTCACCATCTCGGGACCATCATGAAGATCGGCATCGAGCCAA 859
Db 996 GATTATCAGCGACCTAATGACAATCATTTGGCTCCATATTTAAATGAAATCAAAGCAA 1055
QY 860 GAACTTGGGAGTACGACGCTGTGAGCATCTCTCGGACCTCTCGGACCTGACGCTGTGTG 919
Db 1056 GAACTCTACAAATATGATCTCTGACGCAATTTCTTGGAACTCTACGCTCTTGGTTG 1115
QY 920 GGTGGCGTGATCCGCTACCTGACCTTCTTCCACAACACTACAATATCCTCATCGCCACT 979
Db 1116 GGTGGAGTCAATCAGATACCTGGGTTATTTCCAGGCATATAATGATGATTTTAAACAAT 1175
QY 980 GCGGTGGCCCTGCCAGCGTCATGCGTCTTCTGCTGCTGCGTGGTGTCTCATCTACCTGG 1039
Db 1176 GCAGGCCTCACTGCCAAAAGTTCTTCCGTTTGTGCTTGTGCTGCTGATGATTTATCTGG 1235
QY 1040 CTACTGCTTCTGTGGTGGATCGTGTGCTGGGCGCTTATCATGTGAAGTT 1087
Db 1236 TTACACATTTCTGTGGTGGATTTCTTAGGACCATACCATGACAAGTT 1283

RESULT 14
US-10-305-810-4
; Sequence 4, Application US/10305810
; Publication No. US20030176385A1
; GENERAL INFORMATION:
; APPLICANT: Ju, Jingfang
; APPLICANT: Huang, Chunli
; APPLICANT: Zhong, Haihong
; APPLICANT: Simons, Jan Fredrik
; APPLICANT: Tailon, Bruce E.
; APPLICANT: Chant, John S.
; APPLICANT: Peyman, John A.
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN EXPRESSION
; FILE REFERENCE: 21402-501
; CURRENT APPLICATION NUMBER: US/10/305,810
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/334,148
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/336,572
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/625,634
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/192,838
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/194,256
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/970,813
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/182,637
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/240,316
; PRIOR FILING DATE: 2000-10-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 4
; LENGTH: 1677
; TYPE: DNA
; ORGANISM: Ion Transport Channel (Ag 1987)
US-10-305-810-4

Query Match 16.7%; Score 183.8; DB 12; Length 1677;
Best Local Similarity 56.3%; Pred. No. 2e-41;
Matches 388; Conservative 0; Mismatches 292; Indels 9; Gaps 2;

```
QY 399 TTCCACAAGCTGGTCAATGTCAACCATCCACTTCCGGGTGAAGACCAATTAACCTCCAGAGC 458
Db 586 TTATTCAGGCTCTTACAGGTTGAAATCTCCTTTCATCTTAAAGGCATTGACCTACAGACA 645
QY 459 CTCATCAATAATGAGATCCCGGACTGCTATACCTTCAGCGTCTCTGATCACGTTTGACAAC 518
Db 646 ATTCAATCCCGTGAGTTACAGAGCTGTTATGTCTTTTTCAGAAATACGATTATCTTTGACAT 705
QY 519 AAAGCACACAGTGGCGGATCCCCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGT 578
Db 706 AAAGCTCACAGTGGCAAAATCAAAATCTATTTTGACAGTGAATGCCAAATGAAGAATGT 765
QY 579 AAGCACCCAGTGTCTTCCAGCACGGAGACAACAGCTTCCGGCTCCTGTTGACGTGGTG 638
Db 766 AAAGACTTGAACATATT-----TGGATCTAGTAAGTATGCTCTGGTGTGATGCAATTT 819
QY 639 GTCATCCTCACCTGCTCCTGCTCCTTCTCCTCTGCGGCCGCTCACTCCTTCGAGGCTTC 698
Db 820 GTCATTGTGATTTGCTTGGCAATCTCTTATCTGTGTACAAGATCCATTGTTTGTCTCTA 879
QY 699 CTGCTGCAGAACGAGTTTGTGGGGTTTCATGTGGCGGCAGCGGGACGGGTCAATCAGCCTG 758
Db 880 AGGTACCGA---GATTTCTAAATTTCTTCTCGAGAAGTACAAGCGGCTGTGTGTGAC 936
QY 759 TGGGAGCGGCTGGAATTTGTCAATGGCTGGTATACCTCTGCTGTCACAGCGGATGTGCTC 818
Db 937 ACCGACCAAGTGGGAGTTTCATCAACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 996
QY 819 ACCATCTCGGACCATCATCAATGAAGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGAC 878
Db 997 ACAATCATTTGGCTCCATATTAATAATGGAATCAAGCAAGAAATCTCACAACATATGAT 1056
QY 879 GTCTGCAGCATCCTCTCGGACCTCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 938
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QY 999 GTCATGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1058
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Db 1237 ATTGTCTTAGGACCATACCATCTACAGTT 1265
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RESULT 15

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US-10-114-153-21
; Sequence 21, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
```

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; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC AC
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 21
; LENGTH: 1677
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(1645)
US-10-114-153-21
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Query Match 16.7%; Score 183.8; DB 12; Length 1677;
Best Local Similarity 56.3%; Pred. No. 2e-41;
Matches 388; Conservative 0; Mismatches 292; Indels 9; Gaps 2;

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Db 706 AAAGCTCACAGTGGCAAAATCAAAATCTATTTTGACAGTATGCTGCTGCTGCTGCTGCTGCT 765
QY 579 AAGCACCCAGTGTCTTCCAGACGGAGACAACAGCTTCCGGCTCCTGTTGACGTGGTG 638
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Db	1177	GTTCTTCGGTTTGTGCTTGTGCTGGTATGATTATCTGGGTTACACATTCTGTGGCTGG	1236
QY	1059	ATCGTGTCTGGGGCCCTATCATGTGAAGTT	1087
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Job time : 364.801 secs

GenCore version 5.1.6.
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:28:31 ; Search time 357.835 Seconds
(without alignments)
8305.735 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1101	100.0	1740	24	ABL40755
2	1101	100.0	1740	24	AAI71700
3	1101	100.0	2095	24	ABL40754
4	1101	100.0	2095	24	AAI71699
5	1100.6	100.0	2092	24	ABL90358
6	1100.2	99.9	2094	21	AAA39067
7	1099.4	99.9	2052	22	AAF81753
8	1099	99.8	1741	22	AAI59236

C	9	1032.4	93.8	1619	22	AAI61022	Human polynucleoti
	10	851.4	77.3	1827	24	ABL35079	Murine cDNA isolat
	11	642.2	58.3	2092	23	AAS72274	DNA encoding novel
	12	539.6	49.0	734	24	ABL89699	Human polynucleoti
	13	458	41.6	499	23	AAS72273	DNA encoding novel
C	14	334	30.3	635	23	AAS89318	DNA encoding novel
	15	282.8	25.7	776	23	AAS65931	DNA encoding novel
	16	279.8	25.4	361	22	AAK62222	Human immune/haema
	17	260.8	23.7	1762	22	AAH14814	Human cDNA sequenc
	18	244.8	22.2	2860	23	AAS65933	DNA encoding novel
	19	203.8	18.5	1912	22	AAS01697	Human TANGO 480 CD
	20	199.8	18.1	1671	25	ABX56272	Human NOV9b CG9070
	21	199.8	18.1	2067	25	ABX56274	Human NOV9d CG9070
	22	199.8	18.1	2130	25	ABX56273	Human NOV9c CG9070
	23	183.8	16.7	1677	25	ABX56271	Human NOV9a CG9070
	24	169	15.3	11365	22	AAK73827	Human immune/haema
	25	159.6	14.5	20046	22	AAK73826	Human immune/haema
	26	121.2	11.0	2194	23	ABL29717	Drosophila melanog
	27	107.8	9.8	492	22	ABA08523	Human secreted pro
	28	104.8	9.5	318	23	AAS89310	DNA encoding novel
	29	84.8	7.7	5035	23	ABL29716	Drosophila melanog
	30	78	7.1	415	22	AAK58837	Human immune/haema
	31	70	6.4	830	22	AAH07490	Human cDNA clone (
C	32	62	5.6	1296	24	ABQ67797	Listeria innocua D
	33	62	5.6	1311	24	ABQ67800	Listeria innocua D
C	34	62	5.6	319630	24	ABQ67194	Listeria innocua c
	35	62	5.6	3011208	24	ABQ69245	Listeria innocua D
	36	58.4	5.3	319	22	AAD20248	Rat integrin modul
	37	57.4	5.2	2944528	24	ABA03041	Listeria monocytog
	38	56	5.1	12411	24	ABX91613	Modified HIV prote
	39	55.8	5.1	13095	25	ABX07542	S. pneumoniae type
C	40	55.8	5.1	13152	25	ABX07541	S. pneumoniae type
	41	55.8	5.1	14328	25	ABX07543	S. pneumoniae type
C	42	55.8	5.1	2162598	25	ABS56454	Streptococcus pneu
	43	55.6	5.0	2940	21	AAA36699	Humanised F-RSV/HN
	44	55.6	5.0	3106	21	AAA36696	Humanised F-RSV/HN
	45	54	4.9	2634	19	AAV23480	Pseudomonas Orfv s

ALIGNMENTS

RESULT 1
ABL40755
ID ABL40755 standard; cDNA; 1740 BP.
XX
AC ABL40755;
XX
DT 03-JUL-2002 (first entry)
DE Human TLCC-2 protein coding sequence.
XX
KW Transient receptor potential like calcium channel; TRP; TLCC-2; human;
KW neuroprotective; analgesic; nootropic; antiparkinsonian; antidepressant;
KW cerebroprotective; anxiolytic; antimanic; anticonvulsant; gene therapy;
KW calcium signaling; gene; ss.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 1..1740
FT /*tag= a
FT /product= "TLCC-2"
FT /note= "transient receptor potential-like calcium channel"
FT
XX
PN US2002035056-A1.
XX
PD 21-MAR-2002.
XX
PF 06-APR-2001; 2001US-0828466.
XX
PR 07-APR-2000; 2000US-0544797.

XX (CURT/) CURTIS R A J.
PA (SILO/) SILOS-SANTIAGO I.
XX
PI Curtis RAJ, Silos-Santiago I;
XX
DR WPI; 2002-338931/37.
DR P-PSDB; ABB07816.
XX
PT New nucleic acid designated TLCC-2 encodes a transient receptor
PT potential-like calcium channel and is useful to diagnose and treat pain
PT disorders and central nervous system neurodegenerative and neurological
PT disorders
XX
PS Claim 1; Fig 1A-B; 70pp; English.
XX
CC The invention relates to a novel transient receptor potential (TRP)-like
CC calcium channel, designated TLCC-2 and polynucleotides encoding the
CC TLCC-2. TLCC-2 can be expressed by standard recombinant methodology. The
CC TLCC-2 polypeptide, polynucleotides and modulators are useful for
CC treating central nervous system disorders such as neurodegenerative
CC disorders for example Alzheimer's disease, Parkinson's disease, multiple
CC sclerosis, amyotrophic lateral sclerosis, progressive supranuclear palsy,
CC epilepsy, Creutzfeldt-Jakob disease, AIDS-related dementia, familial
CC infantile convulsions, paroxysmal choreoathetosis, psychiatric disorders
CC such as depression, anxiety, schizophrenia, psychoses, mania or phobic
CC disorders, learning or memory disorders such as amnesia, age-related
CC memory loss, or a neurological disorder such as migraine. The molecules
CC are also useful to treat a pain disorder. The present sequence represents
CC the coding sequence of the human TLCC-2 polypeptide.
XX
SQ Sequence 1740 BP; 319 A; 578 C; 475 G; 368 T; 0 other;

Query Match 100.0%; Score 1101; DB 24; Length 1740;
Best Local Similarity 100.0%; Pred. No. 1.8e-239;
Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTCCGGGAAGAGAACACCATCGCCTTCCGACACTCTTCTGCTGGGCTACTCGGACG 60
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|||
QY 61 GAGCGGATGACACCTTCGAGCGCTACACGGGGAGAGCTGTACCGGCCATCTTCCATG 120
Db |||||||
335 GAGCGGATGACACCTTCGAGCGCTACACGGGGAGAGCTGTACCGGCCATCTTCCATG 394
|||
QY 121 CTGTGGACAGTACCTGGCGTTCCTGACGTGCTACCTGGCGCGGTATGCTATGTCCTG 180
Db |||||||
395 CTGTGGACAGTACCTGGCGTTCCTGACGTGCTACCTGGCGCGGTATGCTATGTCCTG 454
|||
QY 181 GTGGGGGTGACCCCTTGGACCAATGGCTCAGGGCTTCTCTCTGCCAGCGGTACTACCAC 240
Db |||||||
455 GTGGGGGTGACCCCTTGGACCAATGGCTCAGGGCTTCTCTCTGCCAGCGGTACTACCAC 514
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QY 241 GAGGCCACGTGGACCCGGCCAAACGACACATTTGACATTCGATCCGATGGTGGTACTGACT 300
Db |||||||
515 GAGGCCACGTGGACCCGGCCAAACGACACATTTGACATTCGATCCGATGGTGGTACTGACT 574
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QY 301 GCATCCAGGTGGATCCCCCGAGCGGCCCTTCCGCCCCCAGCGACGATCTCACCCCTCT 360
Db |||||||
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|||
QY 361 TGAAAGCAGCTCCAGTTACAAGAACCTCACGCTCAAATTCACAAAGCTGGTCAATGTCA 420
Db |||||||
635 TGAAAGCAGCTCCAGTTACAAGAACCTCACGCTCAAATTCACAAAGCTGGTCAATGTCA 694
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QY 421 CCATCCACTTCCGGCTGAAGACCAATTAACCTCCAGAGCCTCATCAATATGAGATCCCGG 480
Db |||||||
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QY 481 ACTGCTATACCTTCAGCGTCTGTATCACGTTTGAACAACAAAGCACACAGTGGCGGATCC 540
Db |||||||
755 ACTGCTATACCTTCAGCGTCTGTATCACGTTTGAACAACAAAGCACACAGTGGCGGATCC 814
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QY 541 CCATCAGCCTGGAGACCCAGGCCCCACATCCAGGAGTGTAAAGCACCCAGTGTCTTCCAGC 600
Db |||||||
815 CCATCAGCCTGGAGACCCAGGCCCCACATCCAGGAGTGTAAAGCACCCAGTGTCTTCCAGC 874
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QY 601 ACGGAGACAACAGCTTCCGGCTCCTGTTTGACCTGGTGGTTCATCTCCTGCTCCCTGT 660
Db |||||||
875 ACGGAGACAACAGCTTCCGGCTCCTGTTTGACCTGGTGGTTCATCTCCTGCTCCCTGT 934
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Db |||||||
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Db |||||||
995 GATTTCATGTGGCGGACGGGGACGGGTTCATCAGCCTGTGGGAGCGGCTGGAATTTGTCA 1054
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Db |||||||
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QY 841 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGATCCTCCTGGGCA 900
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QY 901 CCTCGACGCTGCTGTGTGGTGGCGGTGATCCGCTACCTGACCTTCTTCCACAATACA 960
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QY 1021 TGGCTGTATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGTGGGCGCTATCATG 1080
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1295 TGGCTGTATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGTGGGCGCTATCATG 1354
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QY 1081 TGAAGTTCCGCTCACTCTCCA 1101
Db |||||||
1355 TGAAGTTCCGCTCACTCTCCA 1375
|||
RESULT 2
AAI71700
ID AAI71700 standard; cDNA; 1740 BP.
XX
AC AAI71700;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human TRP-like calcium channel TLCC-2 coding sequence #2.
XX
KW Human; TLCC-2; TRP-like calcium channel; membrane excitability;
KW nociception; nootropic; neuroprotective; antiparkinsonian; cytostatic;
KW hypotensive; antidepressant; analgesic; anticonvulsant; tranquiliser;
KW Parkinson's disease; Huntington's disease; multiple sclerosis;
KW Gilles de la Tourette's syndrome; autonomic function disorder; cancer;
KW neuroleptic; gene therapy; Alzheimer's disease; CNS disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1740
FT /*tag= a
FT /product= "TLCC-2"
FT /partial
XX
XX WO200177331-A1.
PN
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-US11442.
XX
PR 07-APR-2000; 2000US-0544797.

XX (MILL-) MILLENIUM PHARM INC.
PA Curtis RAJ, Silos-Santiago I;
XX WPI; 2002-010913/01.
DR P-PSDB; AAM51858.
XX Novel isolated human transient receptor potential-like calcium channel
PT protein-2 useful for treating Alzheimer's disease, depression, amnesia,
PT pain disorder, and cancer -
XX Claim 1; Fig 1; 148pp; English.
XX The present invention relates to the protein and coding sequences of
CC human transient receptor potential (TRP)-like calcium channel protein-2
CC (TLCC-2). The sequences can be used in the treatment of TLCC-2 related
CC disorders, including central nervous system disorders such as
CC Alzheimer's, Parkinson's and Huntington's diseases, multiple sclerosis,
CC Gilles de la Tourette's syndrome, autonomic function disorders, learning
CC or memory disorders, pain disorders and disorders of cellular
CC proliferation, including cancer. The present sequence is the TLCC-2
CC coding sequence.
XX Sequence 1740 BP; 319 A; 578 C; 475 G; 368 T; 0 other;
Query Match 100.0%; Score 1101; DB 24; Length 1740;
Best Local Similarity 100.0%; Pred. No. 1.8e-239;
Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTTCTCCTGCTGGGCTACTCGGAGC 60
Db 275 CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTTCTCCTGCTGGGCTACTCGGAGC 334
QY 61 GAGCGGATGACACCTTCGAGCCTACACGGGAGCAGCTGTACCAAGCCATCTTCCATG 120
Db 335 GAGCGGATGACACCTTCGAGCCTACACGGGAGCAGCTGTACCAAGCCATCTTCCATG 394
QY 121 CTGTGGACCAAGTACCTGGCGTTGCCTGACGTGTCACTGGGCGGTATGCGTATGTCGGTG 180
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QY 181 GTGGGGGTGACCCCTTGACCAATGGCTCAGGGTTGTCTCTGCCAGCGGTACTACCACC 240
Db 455 GTGGGGGTGACCCCTTGACCAATGGCTCAGGGTTGTCTCTGCCAGCGGTACTACCACC 514
QY 241 GAGGCCACGTGGACCCGCCCAACGACACATTTGACATTGATCCGATGGTGGTTACTGACT 300
Db 515 GAGGCCACGTGGACCCGCCCAACGACACATTTGACATTGATCCGATGGTGGTTACTGACT 574
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Db 635 TGGAAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAATTCACAAGCTGGTCAATGTCA 694
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QY 481 ACTGCTATACCTTCAGCGTCTGTATCACGTTTGACAACAAGCACACAGTGGCGGATCC 540
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Db 815 CCATCAGCCTGGAGACCCAGGCCACATCCAGAGTGAAGCACCCAGTGTCTTCCAGC 874
QY 601 ACGGAGACAACAGCTTCGGGCTCCTGTTTGACGTGGTGGTTCATCTCACCTGCTCCCTGT 660
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Db 1115 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCCTCCTGGGCA 1174
QY 901 CCTCGACGCTGCTGGTGTGGTGGCGGTGATCCGCTACCTGACCTTCTCCACAACACTACA 960
Db 1175 CCTCGACGCTGCTGGTGTGGTGGCGGTGATCCGCTACCTGACCTTCTCCACAACACTACA 1234
QY 961 ATATCCTCATCGCCACACACTGCGGGTGGCGGTGCGCTATGCGCTTCTGCTGCTGCG 1020
Db 1235 ATATCCTCATCGCCACACACTGCGGGTGGCGGTGCGCTATGCGCTTCTGCTGCTGCG 1294
QY 1021 TGGCTGTATCATCTACCTGGGCTACTGCTTCTGCTGGTGGATCGTGGGCGCCCTATCATG 1080
Db 1295 TGGCTGTATCATCTACCTGGGCTACTGCTTCTGCTGGTGGATCGTGGGCGCCCTATCATG 1354
QY 1081 TGAAGTTCCGCTCACTCTCCA 1101
Db 1355 TGAAGTTCCGCTCACTCTCCA 1375
RESULT 3
ABL40754
ID ABL40754 standard; cDNA; 2095 BP.
XX
AC ABL40754;
DT 03-JUL-2002 (first entry)
XX
DE Human TLCC-2 protein encoding cDNA.
XX
KW Transient receptor potential like calcium channel; TRP; TLCC-2; human;
KW neuroprotective; analgesic; nootropic; antiparkinsonian; antidepressant;
KW cerebroprotective; anxiolytic; antimanic; anticonvulsant; gene therapy;
KW calcium signaling; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 141..1883
FT /*tag= a
FT /product= "TLCC-2"
FT /note= "transient receptor potential-like calcium channel"
XX
PN US2002035056-A1.
XX
PD 21-MAR-2002.
XX
PF 06-APR-2001; 2001US-0828466.
XX
PR 07-APR-2000; 2000US-0544797.
XX
PA (CURT/) CURTIS R A J.
PA (SILO/) SILOS-SANTIAGO I.
XX
PI Curtis RAJ, Silos-Santiago I;
XX
DR WPI; 2002-338931/37.
DR P-PSDB; ABB07816.

XX New nucleic acid designated TLCC-2 encodes a transient receptor
PT potential-like calcium channel and is useful to diagnose and treat pain
PT disorders and central nervous system neurodegenerative and neurological
PT disorders -
XX
PS Claim 1; Fig 1A-B; 70pp; English.
XX
CC The invention relates to a novel transient receptor potential (TRP)-like
CC calcium channel, designated TLCC-2 and polynucleotides encoding the
CC TLCC-2. TLCC-2 can be expressed by standard recombinant methodology. The
CC TLCC-2 polypeptide, polynucleotides and modulators are useful for
CC treating central nervous system disorders such as neurodegenerative
CC disorders for example Alzheimer's disease, Parkinson's disease, multiple
CC sclerosis, amyotrophic lateral sclerosis, progressive supranuclear palsy,
CC epilepsy, Creutzfeldt-Jakob disease, AIDS-related dementia, familial
CC infantile convulsions, paroxysmal choreoathetosis, psychiatric disorders
CC such as depression, anxiety, schizophrenia, psychoses, mania or phobic
CC disorders, learning or memory disorders such as amnesia, age-related
CC memory loss, or a neurological disorder such as migraine. The molecules
CC are also useful to treat a pain disorder. The present sequence represents
CC a cDNA encoding the human TLCC-2 polypeptide.
XX
SQ Sequence 2095 BP; 388 A; 682 C; 594 G; 431 T; 0 other;

Query Match 100.0%; Score 1101; DB 24; Length 2095;
Best Local Similarity 100.0%; Pred. No. 1.9e-239;
Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCTGCTGGGCTACTCGGAGC 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
415 CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCTGCTGGGCTACTCGGAGC 474

Qy 61 GAGCGGATGACACCTTCGAGCCTACACGCGGAGCAGCTGTACCAGGCCATCTTCCATG 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
475 GAGCGGATGACACCTTCGAGCCTACACGCGGAGCAGCTGTACCAGGCCATCTTCCATG 534

Qy 121 CTGTGGACAGTACCTGGCGTTCCTGACGTGTACTGGGCGGATGCGTATGTCGCTG 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
535 CTGTGGACAGTACCTGGCGTTCCTGACGTGTACTGGGCGGATGCGTATGTCGCTG 594

Qy 181 GTGGGGTGACCCCTTGGACCAATGGCTCAGGGCTTCTCTGCCAGCGGTACTACCACC 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
595 GTGGGGTGACCCCTTGGACCAATGGCTCAGGGCTTCTCTGCCAGCGGTACTACCACC 654

Qy 241 GAGGCCACGTGGACCCGGCCACGACACATTTGACATTCATCCGATGGTGGTACTGACT 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
655 GAGGCCACGTGGACCCGGCCACGACACATTTGACATTCATCCGATGGTGGTACTGACT 714

Qy 301 GCATCCAGGTGGATCCCCCGAGCGGCCCTTCCGCCCCCCCAGGACGATCTCACCTCT 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
715 GCATCCAGGTGGATCCCCCGAGCGGCCCTTCCGCCCCCCCAGGACGATCTCACCTCT 774

Qy 361 TGGAAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAATTTCCAAGTGGTCAATGTCA 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
775 TGGAAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAATTTCCAAGTGGTCAATGTCA 834

Qy 421 CCATCCACTTCCGGCTGAAGACCAATTAACCTCCAGAGCCTCATCAATATGAGATCCCGG 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
835 CCATCCACTTCCGGCTGAAGACCAATTAACCTCCAGAGCCTCATCAATATGAGATCCCGG 894

Qy 481 ACTGCTATACCTTCAGCGTCTGTATCAGTTTGGACAACAAGCACACAGTGGCGGATCC 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
895 ACTGCTATACCTTCAGCGTCTGTATCAGTTTGGACAACAAGCACACAGTGGCGGATCC 954

Qy 541 CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGTAAAGCACCCTTCTTCCAGC 600
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
955 CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGTAAAGCACCCTTCTTCCAGC 1014

Qy 601 ACGGAGACAAACAGCTTCCGGTCTCTGTTTACGTGGTGGTTCATCTCACCTGCTCCCTGT 660
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1015 ACGGAGACAAACAGCTTCCGGTCTCTGTTTACGTGGTGGTTCATCTCACCTGCTCCCTGT 1074

Qy 661 CTTTCTCTCTCTCGCGCCCGCTCACTCTCTCGAGGGCTTCTGTCTGACAGAGAGTTGTGG 720
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1075 CTTTCTCTCTCTCGCGCCCGCTCACTCTCTCGAGGGCTTCTGTCTGACAGAGAGTTGTGG 1134

Qy 721 GGTTCATGTGGCGGACAGCGGGACGGGTTCATCAGCCTGTGGAGCGGCTGGAATTGTCA 780
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1135 GGTTCATGTGGCGGACAGCGGGACGGGTTCATCAGCCTGTGGAGCGGCTGGAATTGTCA 1194

Qy 781 ATGGCTGTACATCTCTGTCTGTCTACCGAGCGATGTCTACCATCTCGGGCACCATCATGA 840
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1195 ATGGCTGTACATCTCTGTCTGTCTACCGAGCGATGTCTACCATCTCGGGCACCATCATGA 1254

Qy 841 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGAGCATCTCTCTGGGCA 900
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1255 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGAGCATCTCTCTGGGCA 1314

Qy 901 CCTCGACGCTGCTGGTGTGGGTGGGCTGATCCGCTACCTGACCTTCTTCCACAATACA 960
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1315 CCTCGACGCTGCTGGTGTGGGTGGGCTGATCCGCTACCTGACCTTCTTCCACAATACA 1374

Qy 961 ATATCTCATATCGCCACACTGCGGGTGGCCCTGCCCAGCGTATCGGCTTCTGTGCTGCG 1020
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1375 ATATCTCATATCGCCACACTGCGGGTGGCCCTGCCCAGCGTATCGGCTTCTGTGCTGCG 1434

Qy 1021 TGGCTGTATCTACCTGGGCTACTGCTTCTGTGGTGGATCGTGGGGCCCTATCATG 1080
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1435 TGGCTGTATCTACCTGGGCTACTGCTTCTGTGGTGGATCGTGGGGCCCTATCATG 1494

Qy 1081 TGAAGTTCCGCTCACTCTCCA 1101
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1495 TGAAGTTCCGCTCACTCTCCA 1515

RESULT 4
AAI71699
ID AAI71699 standard; cDNA; 2095 BP.
XX
AC AAI71699;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human TRP-like calcium channel TLCC-2 coding sequence #1.
XX
KW Human; TLCC-2; TRP-like calcium channel; membrane excitability;
KW nociception; nootropic; neuroprotective; antiparkinsonian; cyostatic;
KW hypotensive; antidepressant; analgesic; anticonvulsant; tranquiliser;
KW Parkinson's disease; Huntington's disease; multiple sclerosis;
KW Gilles de la Tourette's syndrome; autonomic function disorder; cancer;
KW neuroleptic; gene therapy; Alzheimer's disease; CNS disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 141..1883
FT /*tag= a
FT /product= "TLCC-2"
XX
PN WO200177331-A1.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-US11442.
XX
PR 07-APR-2000; 2000US-0544797.
XX
PA (MILL-) MILLENIUM PHARM INC.
XX
PI Curtis RAJ, Silos-Santiago I;
XX
DR WPI; 2002-010913/01.
DR P-PSDB; AAM51858.
XX
PT Novel isolated human transient receptor potential-like calcium channel

PT protein-2 useful for treating Alzheimer's disease, depression, amnesia,
PT pain disorder, and cancer -
XX
PS Claim 1; Fig 1; 148pp; English.
XX
CC The present invention relates to the protein and coding sequences of
CC human transient receptor potential (TRP)-like calcium channel protein-2
CC (TLCC-2). The sequences can be used in the treatment of TLCC-2 related
CC disorders, including central nervous system disorders such as
CC Alzheimer's, Parkinson's and Huntington's diseases, multiple sclerosis,
CC Gilles de la Tourette's syndrome, autonomic function disorders, learning
CC or memory disorders, pain disorders and disorders of cellular
CC proliferation, including cancer. The present sequence is the TLCC-2
CC coding sequence including the 3' UTR.
XX
SQ Sequence 2095 BP; 388 A; 682 C; 594 G; 431 T; 0 other;
Query Match 100.0%; Score 1101; DB 24; Length 2095;
Best Local Similarity 100.0%; Pred. No. 1.9e-239;
Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATTCCGGGAAGAGACACCATCGCCTTCCGACACCTCTTCCCTGCTGGGCTACTCGGACG 60
Db |||||
QY 415 CATTCCGGGAAGAGACACCATCGCCTTCCGACACCTCTTCCCTGCTGGGCTACTCGGACG 474
Db |||||
QY 61 GAGCGGATGACACCTTCGACGCCCTACACGGGGAGCAGCTGTACCGGCCATCTTCCATG 120
Db |||||
QY 475 GAGCGGATGACACCTTCGACGCCCTACACGGGGAGCAGCTGTACCGGCCATCTTCCATG 534
Db |||||
QY 121 CTGTGGACCAATACCTTGGCGGTTGCCTGACGTGACCTGGCCGGTATGCGTATGTCGGTG 180
Db |||||
QY 535 CTGTGGACCAATACCTTGGCGGTTGCCTGACGTGACCTGGCCGGTATGCGTATGTCGGTG 594
Db |||||
QY 181 GTGGGGGTGACCCCTTGACCAATGGCTCAGGGTGTCTCTGCGCAGCGGTACTACCACC 240
Db |||||
QY 595 GTGGGGGTGACCCCTTGACCAATGGCTCAGGGTGTCTCTGCGCAGCGGTACTACCACC 654
Db |||||
QY 241 GAGGCCACGTGGACCCGGCAACGACACATTTGACATTTGATCCGATGGTGGTTACTGACT 300
Db |||||
QY 655 GAGGCCACGTGGACCCGGCAACGACACATTTGACATTTGATCCGATGGTGGTTACTGACT 714
Db |||||
QY 301 GCATCCAGGTGGATCCCCCGAGCGGGCCCCCTCCGCCCCCCCAGCGACGATCTCACCCCTCT 360
Db |||||
QY 715 GCATCCAGGTGGATCCCCCGAGCGGGCCCCCTCCGCCCCCCCAGCGACGATCTCACCCCTCT 774
Db |||||
QY 361 TGGAAAGCAGCTCCAGTTACAAGAACCTCACGGCTCAAATTTCCACAAGTGGTCAATGTCA 420
Db |||||
QY 775 TGGAAAGCAGCTCCAGTTACAAGAACCTCACGGCTCAAATTTCCACAAGTGGTCAATGTCA 834
Db |||||
QY 421 CCATCCACTTCCGGCTGAAGACCAATTAACCTCCAGAGCCCTCATCAATAGAGATCCCGG 480
Db |||||
QY 835 CCATCCACTTCCGGCTGAAGACCAATTAACCTCCAGAGCCCTCATCAATAGAGATCCCGG 894
Db |||||
QY 481 ACTGCTATACCTTCAGGTCCTGATCACGTTTGACAAACAAAGCACACAGTGGCGGATCC 540
Db |||||
QY 895 ACTGCTATACCTTCAGGTCCTGATCACGTTTGACAAACAAAGCACACAGTGGCGGATCC 954
Db |||||
QY 541 CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGTAAAGCACCCCAAGTGTCTTCCAGC 600
Db |||||
QY 955 CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGTAAAGCACCCCAAGTGTCTTCCAGC 1014
Db |||||
QY 601 ACGGAGACAACAGCTTCCGGCTCCTGTTTGACGTTGGTGTATCCTCACCTGCTCCCTGT 660
Db |||||
QY 1015 ACGGAGACAACAGCTTCCGGCTCCTGTTTGACGTTGGTGTATCCTCACCTGCTCCCTGT 1074
Db |||||
QY 661 CCTTCTCCTCTGCGCCCGGTCACTCCTTCGAGGTTCTCTGTCAGAACAGAGTTTGTGG 720
Db |||||
QY 1075 CCTTCTCCTCTGCGCCCGGTCACTCCTTCGAGGTTCTCTGTCAGAACAGAGTTTGTGG 1134
Db |||||
QY 721 GGTTTCATGTGGCGGACGCGGACCGGTCATCAGCCTGTGGGAGCGGCTGGAATTTGTCA 780
Db |||||
QY 1135 GGTTTCATGTGGCGGACGCGGACCGGTCATCAGCCTGTGGGAGCGGCTGGAATTTGTCA 1194
Db |||||

QY 781 ATGGCTGGTACATCCTGCTCGTCACCGAGGATGTGCTCACCATCTCGGGCACCATCATGA 840
Db |||||
QY 1195 ATGGCTGGTACATCCTGCTCGTCACCGAGGATGTGCTCACCATCTCGGGCACCATCATGA 1254
Db |||||
QY 841 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGAGCATCCTCTCTGGGCA 900
Db |||||
QY 1255 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGAGCATCCTCTCTGGGCA 1314
Db |||||
QY 901 CCTCGACGCTGCTGGTGTGGTGGCGTGTATCCGCTACCTGACCTTCTTCCACAATACA 960
Db |||||
QY 1315 CCTCGACGCTGCTGGTGTGGTGGCGTGTATCCGCTACCTGACCTTCTTCCACAATACA 1374
Db |||||
QY 961 ATATCCTCATCGCCACACTGCGGGTGGCCCTGCCAGCGTCAATGCTGCTGCTGCG 1020
Db |||||
QY 1375 ATATCCTCATCGCCACACTGCGGGTGGCCCTGCCAGCGTCAATGCTGCTGCTGCG 1434
Db |||||
QY 1021 TGGCTGTCACTACCTGGGCTACTGCTTCTGTGGTGGATCGTCTGGGGCCCTATCATG 1080
Db |||||
QY 1435 TGGCTGTCACTACCTGGGCTACTGCTTCTGTGGTGGATCGTCTGGGGCCCTATCATG 1494
Db |||||
QY 1081 TGAAGTTCGCTCACTCTCCA 1101
Db TGAAGTTCGCTCACTCTCCA 1515
RESULT 5
ABL90358
ID ABL90358 standard; cDNA; 2092 BP.
XX
AC ABL90358;
XX
DT 24-MAY-2002 (first entry)
XX
DE Human polynucleotide SEQ ID NO 920.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200190304-A2.
XX
PD 29-NOV-2001.
PF 18-MAY-2001; 2001WO-US16450.
XX
PR 19-MAY-2000; 2000US-205515P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-122018/16.
DR P-PSDB; ABB89949.
XX
PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders -
XX
PS Claim 4; SEQ ID NO 920; 2081pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;

CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2092 BP; 399 A; 676 C; 590 G; 425 T; 2 other;

Query Match 100.0%; Score 1100.6; DB 24; Length 2092;
Best Local Similarity 99.9%; Pred. No. 2.4e-239;
Matches 1100; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTCGGGAAGAGAACACCATCGCTTCCGACACCTCTCTCTGCTGGGCTACTCGGACG 60
Db |||||
382 CATTCGGGAAGAGAACACCATCGCTTCCGACACCTCTCTCTGCTGGGCTACTCGGACG 441

QY 61 GAGCGGATGACACCTTCGCGAGCCTACACGCGGGAGCAGTGTACACGCGCATCTTCCATG 120
Db |||||
442 GAGCGGATGACACCTTCGCGAGCCTACACGCGGGAGCAGTGTACACGCGCATCTTCCATG 501

QY 121 CTGTGGACAGTACCTGGCGGTTGCCTGACGTGTACTGGGCGGATGCGTATGTCGGTG 180
Db |||||
502 CTGTGGACAGTACCTGGCGGTTGCCTGACGTGTACTGGGCGGATGCGTATGTCGGTG 561

QY 181 GTGGGGGTGACCCCTTGGACCAATGGGCTCAGGGCTTGCTCTGCCAGCGGTACTACCACC 240
Db |||||
562 GTGGGGGTGACCCCTTGGACCAATGGGCTCAGGGCTTGCTCTGCCAGCGGTACTACCACC 621

QY 241 GAGGCCAGTGGACCCGCGCAAGACACATTTGACATTGATCCGATGGTGGTTACTGACT 300
Db |||||
622 GAGGCCAGTGGACCCGCGCAAGACACATTTGACATTGATCCGATGGTGGTTACTGACT 681

QY 301 GCATCCAGGTGGATCCCCCGAGGGGCCCCCTCCGCCCCCGAGCGACGATCTACCCCTCT 360
Db |||||
682 GCATCCAGGTGGATCCCCCGAGGGGCCCCCTCCGCCCCCGAGCGACGATCTACCCCTCT 741

QY 361 TGGAAAGCAGCTCCAGTTACAGAACCTCAGCTCAAATTCACAAAGCTGGTCAATGTCA 420
Db |||||
742 TGGAAAGCAGCTCCAGTTACAGAACCTCAGCTCAAATTCACAAAGCTGGTCAATGTCA 801

QY 421 CCATCCACTTCCGGCTGAAGACCAATTAACCTCCAGAGCCTCATCAATAATGAGATCCCGG 480
Db |||||
802 CCATCCACTTCCGGCTGAAGACCAATTAACCTCCAGAGCCTCATCAATAATGAGATCCCGG 861

QY 481 ACTGTATACCTTCAGCGTCTCTGATCAGCTTTTGACAAACAAAGACACAGTGGCGGATCC 540
Db |||||
862 ACTGTATACCTTCAGCGTCTCTGATCAGCTTTTGACAAACAAAGACACAGTGGCGGATCC 921

QY 541 CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGAAGACACCCAGTGTCTTCCAGC 600
Db |||||
922 CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGAAGACACCCAGTGTCTTCCAGC 981

QY 601 ACGGAGACAACAGCTTCCGGCTCCTGTTTGACGTGGTGGTCACTCCTCACCTGCTCCCTGT 660
Db |||||
982 ACGGAGACAACAGCTTCCGGCTCCTGTTTGACGTGGTGGTCACTCCTCACCTGCTCCCTGT 1041

QY 661 CCTTCTCTCTCGCCCGCTCACTCCTTCCGAGGCTTCTGCTGCAGAACGAGTTTGTGG 720
Db |||||
1042 CCTTCTCTCTCGCCCGCTCACTCCTTCCGAGGCTTCTGCTGCAGAACGAGTTTGTGG 1101

QY 721 GGTTCATGTGGCGGACGCGGGACGGGTCACTCAGCCTGTGGGAGCGGTGGAATTTGTCA 780
Db |||||
1102 GGTTCATGTGGCGGACGCGGGACGGGTCACTCAGCCTGTGGGAGCGGTGGAATTTGTCA 1161

QY 781 ATGGCTGGTACATCCTGCTCGTCACCGAGGATGTGCTCACCATCTCGGGACCATCATGA 840
Db |||||
1162 ATGGCTGGTACATCCTGCTCGTCACCGAGGATGTGCTCACCATCTCGGGACCATCATGA 1221

QY 841 AGATCGGCATCGAGGCGCCAGAACTTGGCGAGCTACGACGCTGTCAGCATCCTCTCTGGGCA 900
Db |||||
1222 AGATCGGCATCGAGGCGCCAGAACTTGGCGAGCTACGACGCTGTCAGCATCCTCTCTGGGCA 1281

QY 901 CCTCGACGCTGCTGGTGTGGGTGGCGTGTATCCGCTACCTGACCTTCTTCCACAACACTACA 960
Db |||||
1282 CCTCGACGCTGCTGGTGTGGGTGGCGTGTATCCGCTACCTGACCTTCTTCCACAACACTACA 1341

QY 961 ATATCCTCATCGCCACACTCGGGGTGGCCCTGTCGCGAGCGTATGCGCTTCTGCTGCTGCG 1020
Db |||||
1342 ATATCCTCATCGCCACACTCGGGGTGGCCCTGTCGCGAGCGTATGCGCTTCTGCTGCTGCG 1401

QY 1021 TGGCTGTCTATCTACCTGGGCTACTGCTTCTGTGCTGGATCGTGTGGGCGCCCTATCATG 1080
Db |||||
1402 TGGCTGTCTATCTACCTGGGCTACTGCTTCTGTGCTGGATCGTGTGGGCGCCCTATCATG 1461

QY 1081 TGAAGTTCGCTCACTCTCCA 1101
Db |||||
1462 TGAAGTTCGCTCACTCTCCA 1482

RESULT 6
AAA39067
ID AAA39067 standard; cDNA; 2094 BP.
XX
AC AAA39067;
XX
DT 30-AUG-2000 (first entry)
XX
DE Human secreted protein gene 16 SEQ ID NO:26.
XX
KW Human; secreted protein; cytostatic; anti-proliferative; vulnerary;
KW immunosuppressive; antibacterial; diagnosis; immune system; chemotaxis;
KW hyperproliferative disorder; infectious disease; tissue regeneration;
KW screening; food additive; preservative; wound healing;
KW hyper-vascular disease; ss.
XX
OS Homo sapiens.
XX
FN WO200017222-A1.
XX
PD 30-MAR-2000.
XX
PF 22-SEP-1999; 99WO-US22012.
XX
PR 23-SEP-1998; 98US-0101546.
PR 02-OCT-1998; 98US-0102895.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Rosen CA, Duan RD, Shi Y, Lafleur DW, Young PE, Ni J;
PI Komatsoulis G, Endress GA, Soppet DR;
XX
DR WPI; 2000-283538/24.
DR P-PSDB; AAB08906.
XX
PT Human secreted proteins and coding sequences useful in diagnostic and
PT therapeutic methods for disorders such as immune system or
PT proliferative disorders, related to the proteins -
XX
PS Claim 1; Page 331-332; 416pp; English.
XX
CC The polynucleotide sequences given in AAA39052 to AAA39088 encode the
CC human secreted proteins given in AAB08891 to AAB08984. The human secreted
CC proteins can have activities based on the tissues and cells they are
CC expressed in. Examples of the activities are: cytostatic;
CC anti-proliferative; immunosuppressive; antibacterial; and vulnerary. The
CC secreted proteins and their related polynucleotide sequences are useful
CC for diagnostic and therapeutic methods useful for diagnosing and treating
CC disorders related to the secreted proteins. The proteins, and
CC polynucleotide sequences may be useful for treating disorders of the
CC immune system, hyperproliferative disorders, infectious disease,
CC regeneration of tissues, for chemotaxis and for screening molecules that

CC bind to the proteins. The proteins or polynucleotide sequences may be
CC used as food additives or preservatives, to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, co-factors or other nutritional components. Agonists or
CC antagonists of the proteins may be used to prevent scar tissue growth
CC during wound healing, and hyper-vascular diseases. AAA39043 to AAA39051
CC and AAB08890 are sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 2094 BP; 400 A; 673 C; 589 G; 426 T; 6 other;

Query Match 99.9%; Score 1100.2; DB 21; Length 2094;
Best Local Similarity 99.8%; Pred. No. 2.9e-239;
Matches 1099; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCTGCTGGGCTACTCGGACG 60
Db |||||
382 CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCTGCTGGGCTACTCGGACG 441

QY 61 GAGCGGATGACACCTTCGAGCCTACACGGGGAGCAGCTGTACCGGCATCTTCCATG 120
Db |||||
442 GAGCGGATGACACCTTCGAGCCTACACGGGGAGCAGCTGTACCGGCATCTTCCATG 501

QY 121 CTGTGGACCACTACCTGGGTTGCCTGACGTGTCACTGGGCGGTATGCGTATGTCGGTG 180
Db |||||
502 CTGTGGACCACTACCTGGGTTGCCTGACGTGTCACTGGGCGGTATGCGTATGTCGGTG 561

QY 181 GTGGGGGTGACCCCTTGACCAATGGCTCAGGGCTTGCTCTCTGCCAGCGGTACTACCACC 240
Db |||||
562 GTGGGGGTGACCCCTTGACCAATGGCTCAGGGCTTGCTCTCTGCCAGCGGTACTACCACC 621

QY 241 GAGGCCACGTGGACCCGGCCAAACGACACATTTGACATTGATCCGATGGTGGTTACTGACT 300
Db |||||
622 GAGGCCACGTGGACCCGGCCAAACGACACATTTGACATTGATCCGATGGTGGTTACTGACT 681

QY 301 GCATCCAGGTGGATCCCGCGAGCGGCCCTCCGCCCCCAGCGACGATCTCACCCCTCT 360
Db |||||
682 GCATCCAGGTGGATCCCGCGAGCGGCCCTCCGCCCCCAGCGACGATCTCACCCCTCT 741

QY 361 TGGAAAGCAGCTCCAGTTACAAGAACCTCACGCTCAAATTCACAAAGCTGGTCAATGTCA 420
Db |||||
742 TGGAAAGCAGCTCCAGTTACAAGAACCTCACGCTCAAATTCACAAAGCTGGTCAATGTCA 801

QY 421 CCATCCACTTCCGGCTGAGACCACTTAACCTCCAGAGCCTCATCAATATGAGATCCCGG 480
Db |||||
802 CCATCCACTTCCGGCTGAGACCACTTAACCTCCAGAGCCTCATCAATATGAGATCCCGG 861

QY 481 ACTGCTATACCTTCAGGCTCCTGATCACGTTTGACAAACAAAGCACACAGTGGCGGATCC 540
Db |||||
862 ACTGCTATACCTTCAGGCTCCTGATCACGTTTGACAAACAAAGCACACAGTGGCGGATCC 921

QY 541 CCATCAGCCTGGAGACCCAGGCCCCACATCCAGGAGTGAAGCACCCCACTGTCTTCCAGC 600
Db |||||
922 CCATCAGCCTGGAGACCCAGGCCCCACATCCAGGAGTGAAGCACCCCACTGTCTTCCAGC 981

QY 601 ACGGAGACAACAGCTTCGGCTCCTGTTGACGTGGTGCATCCTCACCTGCTCCCTGT 660
Db |||||
982 ACGGAGACAACAGCTTCGGCTCCTGTTGACGTGGTGCATCCTCACCTGCTCCCTGT 1041

QY 661 CTTTCTCCTCTCGGCCGCTCACTCCTTCGAGGCTTCTGCTGCAGAACGAGTTTGTGG 720
Db |||||
1042 CTTTCTCCTCTCGGCCGCTCACTCCTTCGAGGCTTCTGCTGCAGAACGAGTTTGTGG 1101

QY 721 GGTTCATGTGGCGGACGGGGACGGGTGCATCAGCCTGTGGGAGCGGCTGGAATTTGTCA 780
Db |||||
1102 GGTTCATGTGGCGGACGGGGACGGGTGCATCAGCCTGTGGGAGCGGCTGGAATTTGTCA 1161

QY 781 ATGGTGGTACATCTCTGCTCACCAGCGATGTGCTCACCATCTCGGGACCATCATGA 840
Db |||||
1162 ATGGTGGTACATCTCTGCTCACCAGCGATGTGCTCACCATCTCGGGACCATCATGA 1221

QY 841 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACACGCTGTCAGCATCTCTCTGGGCA 900
Db |||||

Db 1222 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTTCGAGCATCTCTCTGGGCA 1281
QY 901 CCTCGACGCTGCTGGTGTGGGTGGCGTGATCCGCTACCTGACCTTCTTCCACAACACTACA 960
Db |||||
1282 CCTCGACGCTGCTGGTGTGGGTGGCGTGATCCGCTACCTGACCTTCTTCCACAACACTACA 1341
QY 961 ATATCTCATCGCCACACTCGGGTGGCCCTGCCAGCGTCAATGCGCTTCTGCTGCTGCG 1020
Db |||||
1342 ATATCTCATCGCCACACTCGGGTGGCCCTGCCAGCGTCAATGCGCTTCTGCTGCTGCG 1401
QY 1021 TGGCTGTCTATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGGGCCCTATCATG 1080
Db |||||
1402 TGGCTGTCTATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGGGCCCTATCATG 1461
QY 1081 TGAAGTTCCGCTCACTCTCCA 1101
Db |||||
1462 TGAAGTTCCGCTCACTCTCCA 1482

RESULT 7
AAF81753
ID AAF81753 standard; cDNA; 2052 BP.
XX
AC AAF81753;
XX
DT 12-JUN-2001 (first entry)
XX
DE Human membrane associated protein MEMAP-13 encoding cDNA.
XX
KW Human; membrane associated protein; MEMAP; diagnosis; cytostatic;
KW antiinflammatory; anticonvulsant; immunosuppressive; antidiarrheic;
KW antiarteriosclerotic; gene therapy; cell proliferative disorder;
KW autoimmune disorder; inflammatory disorder; neurological disorder;
KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;
KW epilepsy; diarrhoea; ss.
XX
OS Homo sapiens.
XX
PN WO200112662-A2.
XX
PD 22-FEB-2001.
XX
PF 14-AUG-2000; 2000WO-US22315.
XX
PR 17-AUG-1999; 99US-0149641.
PR 09-NOV-1999; 99US-0164203.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;
PI Baughn MR, Lu DAM, Patterson C;
XX
DR WPI; 2001-168860/17.
DR P-PSDB; AAB74707.
XX
PT Isolated polypeptide with a human membrane associated protein sequence
PT is useful for the diagnosis, prevention and treatment of cell
PT proliferative, autoimmune/inflammatory, neurological and
PT gastrointestinal disorders -
XX
PS Claim 5; Page 157-158; 173pp; English.
XX
CC AAF81741 to AAF81777 encode the human membrane associated proteins
CC (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,
CC antiinflammatory, anticonvulsant, immunosuppressive, antidiarrheic and
CC antiarteriosclerotic activities, which can be used in gene therapy.
CC MEMAPs and agonist of MEMAPs can be used to treat a disease or condition
CC associated with decreased expression of functional MEMAP and antagonists
CC of MEMAP are used to treat a disease or condition associated with
CC overexpression of functional MEMAP. These disorders include cell
CC proliferative, autoimmune/inflammatory, neurological and gastrointestinal
CC disorders. The MEMAP polynucleotides and proteins are also used for the
CC diagnosis of these disorders. Specific examples of these disorders

CC include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea.
CC MEMAP proteins can be used to screen for compounds which specifically
CC bind MEMAP including antibodies, oligonucleotides, proteins and small
CC molecules. MEMAP polynucleotides can be used to prepare transgenic
CC animals which can be studied to provide information concerning human
CC disease. Anti-MEMAP antibodies are useful in immunoassays for the
CC detection of MEMAP protein and can be used as antagonists to treat or
CC prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
CC can be delivered to target cells with genetic abnormalities with respect
CC to the expression of MEMAP to treat or prevent a disorder associated
CC with MEMAP.
XX
SQ

Sequence 2052 BP; 375 A; 670 C; 582 G; 425 T; 0 other;
Query Match 99.9%; Score 1099.4; DB 22; Length 2052;
Best Local Similarity 99.9%; Pred. No. 4.4e-239;
Matches 1100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCTGCTGGGCTACTCGGACG	60
Db	382	CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCTGCTGGGCTACTCGGACG	441
Qy	61	GAGCGGATGACACCTTCGACGCTACACGCGGGAGAGCTGTACCAGGCCATCTTCCATG	120
Db	442	GAGCGGATGACACCTTCGACGCTACACGCGGGAGAGCTGTACCAGGCCATCTTCCATG	501
Qy	121	CTGTGGACCACTACCTGGCGTTGCCTGACGTGTGACTGGCGCGGTATGCGTATGTCGGTG	180
Db	502	CTGTGGACCACTACCTGGCGTTGCCTGACGTGTGACTGGCGCGGTATGCGTATGTCGGTG	561
Qy	181	GTGGGGGTGACCCCTTGACCAATGGCTCAGGGCTGTCTCTGCCAGCGGTACTACCACC	240
Db	562	GTGGGGGTGACCCCTTGACCAATGGCTCAGGGCTGTCTCTGCCAGCGGTACTACCACC	621
Qy	241	GAGCCACGTGGACCCGGCCAAACGACACATTTGACATTTGATCCGATGGTGTACTGACT	300
Db	622	GAGCCACGTGGACCCGGCCAAACGACACATTTGACATTTGATCCGATGGTGTACTGACT	681
Qy	301	GCATCCAGGTGGATCCCGCCGAGCGGCGCCCTCCGCGCCCGGACGATCTCACCCCTCT	360
Db	682	GCATCCAGGTGGATCCCGCCGAGCGGCGCCCTCCGCGCCCGGACGATCTCACCCCTCT	741
Qy	361	TGGAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAATTCACAAAGCTGGTCAATGTCA	420
Db	742	TGGAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAATTCACAAAGCTGGTCAATGTCA	801
Qy	421	CCATCCACTTCGGGCTGAGACCACTTAACCTCCAGAGCCTCATCAATAGATCCCGG	480
Db	802	CCATCCACTTCGGGCTGAGACCACTTAACCTCCAGAGCCTCATCAATAGATCCCGG	861
Qy	481	ACTGCTATACCTTCAGCGTCTCTGATCAGCTTTGACAAACAAAGCACACAGTGGCGGATCC	540
Db	862	ACTGCTATACCTTCAGCGTCTCTGATCAGCTTTGACAAACAAAGCACACAGTGGCGGATCC	921
Qy	541	CCATCAGCCTGGAGACCCAGGCCCCACATCCAGAGTGTAAAGCACCCAGTGTCTTCCAGC	600
Db	922	CCATCAGCCTGGAGACCCAGGCCCCACATCCAGAGTGTAAAGCACCCAGTGTCTTCCAGC	981
Qy	601	ACGGAGACAACAGCTTCGGGCTCCTGTTTACGCTGGTGGTCACTCCTCAGCTGCTCCCTGT	660
Db	982	ACGGAGACAACAGCTTCGGGCTCCTGTTTACGCTGGTGGTCACTCCTCAGCTGCTCCCTGT	1041
Qy	661	CCTTCCTCCTCTCGCGCCGCTCACTCCTTCGAGGCTTCTGCTGCAGAACGAGTTTGTGG	720
Db	1042	CCTTCCTCCTCTCGCGCCGCTCACTCCTTCGAGGCTTCTGCTGCAGAACGAGTTTGTGG	1101
Qy	721	GGTTTCATGTGGCGGACGGGGACGGGTCACTCAGCCTGTGGGAGCGGTGGAATTTGTCA	780
Db	1102	GGTTTCATGTGGCGGACGGGGACGGGTCACTCAGCCTGTGGGAGCGGTGGAATTTGTCA	1161
Qy	781	ATGGCTGGTACATCTGCTCGTCACTCAGCGATGTCTCACCATCTCGGGCACCATCATGA	840
Db	1162	ATGGCTGGTACATCTGCTCGTCACTCAGCGATGTCTCACCATCTCGGGCACCATCATGA	1221

Qy	841	AGATCGGCATCGAGCCAAAGAACTTGGCGAGCTACGACGTCGTGCGATCCTCCTGGGCA	900
Db	1222	AGATCGGCATCGAGCCAAAGAACTTGGCGAGCTACGACGTCGTGCGATCCTCCTGGGCA	1281
Qy	901	CCTCGACGCTGCTGGTGTGGTGGCGGTGATCCGCTACCTGACCTTCTTCCACAATACA	960
Db	1282	CCTCGACGCTGCTGGTGTGGTGGCGGTGATCCGCTACCTGACCTTCTTCCACAATACA	1341
Qy	961	ATATCCTCATCGCCACACTGCGGGTGGCGCTGCCAGCGTCATGCGCTTCTGCTGTGG	1020
Db	1342	ATATCCTCATCGCCACACTGCGGGTGGCGCTGCCAGCGTCATGCGCTTCTGCTGTGG	1401
Qy	1021	TGGCTGTCTACTGAGCTGGGCTACTGCTTCTGTGGCTGGATCGTGGGGCCCTATCATG	1080
Db	1402	TGGCTGTCTACTGAGCTGGGCTACTGCTTCTGTGGCTGGATCGTGGGGCCCTATCATG	1461
Qy	1081	TGAAGTTCCGCTCACTCTCCA	1101
Db	1462	TGAAGTTCCGCTCACTCTCCA	1482

RESULT 8
AAI59236

ID AAI59236 standard; cDNA; 1741 BP.

XX AC AAI59236;

DT 22-OCT-2001 (first entry)

XX Human polynucleotide SEQ ID NO 1439.

Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
peripheral nervous system; neuropathy; central nervous system; CNS;
Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
leukaemia; ss.

XX Homo sapiens.

OS WO200153312-A1.

XX 26-JUL-2001.

PF 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

DR P-PSDB; AAM40080.

XX Novel nucleic acids and polypeptides, useful for treating disorders
such as central nervous system injuries -

PS Claim 1; SEQ ID NO 1439; 10078pp; English.

CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
the encoded polypeptides (AAM38642-AAM42213) with nootropic,
immunosuppressant and cytostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX

Sequence 1741 BP; 320 A; 554 C; 487 G; 380 T; 0 other;
Query Match 99.8%; Score 1099; DB 22; Length 1741;
Best Local Similarity 100.0%; Pred. No. 5.2e-239;
Matches 1099; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	3	TTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCCTGCTGGCTACTCGGACGGA	62
Db	73	TTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCCTGCTGGCTACTCGGACGGA	132
QY	63	GCGGATGACACCTTCGACGCTACACGGGGAGCAGCTGTACACGCCCATCTTCCATGCT	122
Db	133	GCGGATGACACCTTCGACGCTACACGGGGAGCAGCTGTACACGCCCATCTTCCATGCT	192
QY	123	GTGGACAGTACCTGCGCTTGCCGTGACGTGACGTGCGGCGGATGCGTATGTCGGTGGT	182
Db	193	GTGGACAGTACCTGCGCTTGCCGTGACGTGCGGCGGATGCGTATGTCGGTGGT	252
QY	183	GGGGGTGACCCCTTGACCAATGGCTCAGGGCTGCTCTCTGCCAGGGTACTACCAACCGA	242
Db	253	GGGGGTGACCCCTTGACCAATGGCTCAGGGCTGCTCTCTGCCAGGGTACTACCAACCGA	312
QY	243	GGCCACGTGGACCCGSCCAACGACACATTTGACATGATCCGATGGTGGTTACTGACTGC	302
Db	313	GGCCACGTGGACCCGSCCAACGACACATTTGACATGATCCGATGGTGGTTACTGACTGC	372
QY	303	ATCCAGGTGGATCCCCCGAGCGGCCCCCTCCGCCCCCCAGCGACGATCTCACCCCTCTTG	362
Db	373	ATCCAGGTGGATCCCCCGAGCGGCCCCCTCCGCCCCCCAGCGACGATCTCACCCCTCTTG	432
QY	363	GAAAGCAGCTCCAGTTACAAGAACCTCAAGCTCAAAATTCACAAGCTGGTCAATGTCACC	422
Db	433	GAAAGCAGCTCCAGTTACAAGAACCTCAAGCTCAAAATTCACAAGCTGGTCAATGTCACC	492
QY	423	ATCCACTTCCGGCTGAGACCAATTAACCTCCAGAGCCTCATCAATATGAGATCCCGGAC	482
Db	493	ATCCACTTCCGGCTGAGACCAATTAACCTCCAGAGCCTCATCAATATGAGATCCCGGAC	552
QY	483	TGCTATACCTTCAGGTCCTGATCACGTTTGACAAACAAAGCACACAGTGGCGGATCCCC	542
Db	553	TGCTATACCTTCAGGTCCTGATCACGTTTGACAAACAAAGCACACAGTGGCGGATCCCC	612
QY	543	ATCAGCCTGGAGACCCAGGCCCCACATCCAGGAGTGTAGCACCCCAAGTGTCTTCCAGCAC	602
Db	613	ATCAGCCTGGAGACCCAGGCCCCACATCCAGGAGTGTAGCACCCCAAGTGTCTTCCAGCAC	672
QY	603	GGAGACAACAGCTTCCGGCTCCTGTTTGACGCTGGTGTATCCTCAGCTGCTCCCTGTCC	662
Db	673	GGAGACAACAGCTTCCGGCTCCTGTTTGACGCTGGTGTATCCTCAGCTGCTCCCTGTCC	732
QY	663	TTCCTCCTCTGCGCCCGCTCACTCCTTCGAGGCTTCCTGCTGCAGAACGAGTTTGTGGG	722
Db	733	TTCCTCCTCTGCGCCCGCTCACTCCTTCGAGGCTTCCTGCTGCAGAACGAGTTTGTGGG	792
QY	723	TTCATGTGGCGGACGGGGACGGGTCAATCAGCTGTGGGAGCGGCTGAATTTGTCAAT	782
Db	793	TTCATGTGGCGGACGGGGACGGGTCAATCAGCTGTGGGAGCGGCTGAATTTGTCAAT	852
QY	783	GGCTGGTACATCCTGCTCGTCAACCAAGCGATGTGCTCACCATCTCGGGCACCATCATGAAG	842

Db	853	GGCTGGTACATCCTGCTCGTCACAGCGATGTGCTCACCATCTCGGGCACCATCATGAAG	912
QY	843	ATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCGAGCATCTCCTGGGCACC	902
Db	913	ATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCGAGCATCTCCTGGGCACC	972
QY	903	TCGACGCTGCTGGTGTGGTGGGCGTGATCCGCTACCTGACCTTCTTCCACAACATAAT	962
Db	973	TCGACGCTGCTGGTGTGGTGGGCGTGATCCGCTACCTGACCTTCTTCCACAACATAAT	1032
QY	963	ATCCTCATCGCCACACTGCGGGTGGGCTGCTGCCCCAGCGTCATGCGCTTCTGCTGCTGCTG	1022
Db	1033	ATCCTCATCGCCACACTGCGGGTGGGCTGCTGCCCCAGCGTCATGCGCTTCTGCTGCTGCTG	1092
QY	1023	GCTGTCACTACCTGGGCTACTGCTTCTGTGGCTGGATCGTCTGGGGCCCTATCATGTG	1082
Db	1093	GCTGTCACTACCTGGGCTACTGCTTCTGTGGCTGGATCGTCTGGGGCCCTATCATGTG	1152
QY	1083	AAGTTCGCTCACTCTCCA	1101
Db	1153	AAGTTCGCTCACTCTCCA	1171
RESULT 9			
AAI61022/C			
ID	AAI61022 standard; cDNA; 1619 BP.		
XX			
AC	AAI61022;		
XX			
DT	22-OCT-2001 (first entry)		
XX			
DE	Human polynucleotide SEQ ID NO 5011.		
XX			
KW	Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;		
KW	peripheral nervous system; neuropathy; central nervous system; CNS;		
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;		
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;		
KW	chemokinetic; thrombolytic; drug screening; arthritis; inflammation;		
KW	leukaemia; ss.		
OS	Homo sapiens.		
XX			
PN	WO200153312-A1.		
PD	26-JUL-2001.		
XX			
PF	26-DEC-2000; 2000WO-US34263.		
XX			
PR	21-JAN-2000; 2000US-0488725.		
PR	25-APR-2000; 2000US-0552317.		
PR	09-JUL-2000; 2000US-0598042.		
PR	19-JUL-2000; 2000US-0620312.		
PR	03-AUG-2000; 2000US-0653450.		
PR	14-SEP-2000; 2000US-0662191.		
PR	19-OCT-2000; 2000US-0693036.		
PR	29-NOV-2000; 2000US-0727344.		
XX			
PA	(HYSE-) HYSEQ INC.		
XX			
PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;		
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;		
PI	Zhao QA, Zhou P, Goodrich R, Drmanac RT;		
XX			
DR	WPI; 2001-442253/47.		
DR	P-PSDB; AAM41866.		
XX			
PT	Novel nucleic acids and polypeptides, useful for treating disorders		
PT	such as central nervous system injuries -		
XX			
PS	Claim 1; SEQ ID NO 5011; 10078pp; English.		
XX			
CC	The invention relates to human nucleic acids (AAI57798-AAI61369) and		

CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

XX
SQ Sequence 1619 BP; 350 A; 450 C; 518 G; 301 T; 0 other;

Query Match 93.8%; Score 1032.4; DB 22; Length 1619;
Best Local Similarity 99.8%; Pred. No. 6e-224;
Matches 1044; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy	57	GACGGAGCGGATGACACCTTCGCAGCCTACACGGGGAGCAGCTGTACAGGCCATCTTC	116
Db	1619	GACGGAGCGGATGACACCTTCGCAGCCTACACGGGGAGCAGCTGTACAGGCCATCTTC	1560
Qy	117	CATGCTGTGGACCACTACCTGGCGTTGCCTGACGTGTCACTGGCGCGATGCGTATGTC	176
Db	1559	CATGCTGTGGACCACTACCTGGCGTTGCCTGACGTGTCACTGGCGCGATGCGTATGTC	1500
Qy	177	CGTGGTGGGGTGACCCCTTGGACCAATGGCTCAGSGCTTGCTCTCTGCCAGCGGTACTAC	236
Db	1499	CGTGGTGGGGTGACCCCTTGGACCAATGGCTCAGSGCTTGCTCTCTGCCAGCGGTACTAC	1440
Qy	237	CACCGAGGCCACGTGGACCCGGGCCAACGACACATTTGACATTTGATCCGATGGTGGTTACT	296
Db	1439	CACCGAGGCCACGTGGACCCGGGCCAACGACACATTTGACATTTGATCCGATGGTGGTTACT	1380
Qy	297	GACTGCATCCA-GGTGGATCCCCCGGAGCGGCCCTCCGCCCCCAGCAGCATCTCAC	355
Db	1379	GACTGCATCCAGGTGGATCCCCCGGAGCGGCCCTCCGCCCCCAGCAGCATCTCAC	1320
Qy	356	CCTCTTGGAAAGCAGCTCCAGTTCAAGAACCTCAGCTCAAATTCACAAGCTGGTCAA	415
Db	1319	CCTCTTGGAAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAATTCACAAGCTGGTCAA	1260
Qy	416	TGTCACCATCCACTCCGGGTGAAGACCATTAACCTCCAGAGCCTCATCAATAATGAGAT	475
Db	1259	TGTCACCATCCACTCCGGGTGAAGACCATTAACCTCCAGAGCCTCATCAATAATGAGAT	1200
Qy	476	CCCGGACTGCTATACCTTCAGCGTCTCTGATCAGCTTGACAAACAAAGCACAGTGGCG	535
Db	1199	CCCGGACTGCTATACCTTCAGCGTCTCTGATCAGCTTGACAAACAAAGCACAGTGGCG	1140
Qy	536	GATCCCCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGTAAAGCACCCAGTGTCTT	595
Db	1139	GATCCCCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGTAAAGCACCCAGTGTCTT	1080
Qy	596	CCAGCACGGAGACAACAGCTTCGGGCTCCTGTTGACGTGGTGGTCACTCCTCAGCTGCTC	655
Db	1079	CCAGCACGGAGACAACAGCTTCGGGCTCCTGTTGACGTGGTGGTCACTCCTCAGCTGCTC	1020
Qy	656	CCTGTCCTTCTCCTCTCGGCCGCTCACTCCTTCGAGGCTTCTCTGTCGAGAACGAGTT	715
Db	1019	CCTGTCCTTCTCCTCTCGGCCGCTCACTCCTTCGAGGCTTCTCTGTCGAGAACGAGTT	960
Qy	716	TGTGGGTTTCATGTGGGGCAGCGGGGACGGGTATCAGCCTGTGGGAGCGGCTGGAATT	775
Db	959	TGTGGGTTTCATGTGGGGCAGCGGGGACGGGTATCAGCCTGTGGGAGCGGCTGGAATT	900
Qy	776	TGTCAATGGCTGGTACATCCTGCTCGTCACAGGATGTGCTACCATCTCGGGCACCAT	835
Db	899	TGTCAATGGCTGGTACATCCTGCTCGTCACAGGATGTGCTACCATCTCGGGCACCAT	840

Qy	836	CATGAAGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCCTCCT	895
Db	839	CATGAAGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCCTCCT	780
Qy	896	GGGCACCTCGACCTGCTGGTGTGGGTGGCGGTGATCCGCTACCTGACCTTCTTCCACAA	955
Db	779	GGGCACCTCGACCTGCTGGTGTGGGTGGCGGTGATCCGCTACCTGACCTTCTTCCACAA	720
Qy	956	CTACAATATCCTCATCGCCACACTGCGGGTGGCCCTGCCAGCGTCATGCGTCTTCTGCTG	1015
Db	719	CTACAATATCCTCATCGCCACACTGCGGGTGGCCCTGCCAGCGTCATGCGTCTTCTGCTG	660
Qy	1016	CTGCGTGGCTGTCACTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGGGGCCCTA	1075
Db	659	CTGCGTGGCTGTCACTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGGGGCCCTA	600
Qy	1076	TCATGTGAAGTTCGGCTCACTCTCCA	1101
Db	599	TCATGTGAAGTTCGGCTCACTCTCCA	574

RESULT 10

ABL35079

ID ABL35079 standard; cDNA; 1827 BP.

XX ABL35079;

DT 04-APR-2002 (first entry)

XX Murine cDNA isolated from skin cells SEQ ID NO: 608.

DE Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
XX developmental defect; inflammatory disease; dermatological; vulnery;
KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
KW ss.

OS Mus sp.

XX WO200190357-A1.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-NZ00099.

XX 24-MAY-2000; 2000US-206650P.

XX 25-JUL-2000; 2000US-221232P.

PA (GENE-) GENESIS RES & DEV CORP LTD.

XX Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD;
PI WPI; 2002-122020/16.
XX P-PSDB; ABB72389.

XX New polynucleotides and polypeptides encoded by the polynucleotides
PT isolated from skin cells, useful for treating skin wounds, cancers,
PT growth and developmental defects, inflammatory diseases, or for
PT modulating immune responses -

PS Claim 1; Page 379-380; 466pp; English.

XX The present invention provides the protein and coding sequences of cDNAs
CC isolated from human, murine and rat skin cell libraries. The sequences
CC can be used in the development of therapeutic agents useful in the
CC treatment of skin diseases, including skin wounds, cancer, growth
CC defects, developmental defects and inflammatory diseases. The proteins
CC have important roles in the induction of hair growth, cell proliferation
CC and cell-cell interaction, in maintaining tissue integrity, in wound
CC healing and in modulating immune responses. The present sequence is a
CC cDNA of the invention.

XX Sequence 1827 BP; 392 A; 507 C; 469 G; 459 T; 0 other;

Query Match		77.3%;	Score 851.4;	DB 24;	Length 1827;
Best Local Similarity		85.8%;	Pred. No. 5.5e-183;		
Matches 945;		Conservative 0;	Mismatches 156;	Indels 0;	Gaps 0;
QY	1	CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCCCTGCTGGGCTACTCGGACG	60		
Db	167	CATTCCGGGAAGAGAACACCATTGCCTTCCGACATCTCTTCCCTGCTGGGTTACTCTGATG	226		
QY	61	GAGCGGATGACACCTTCGACGCTACACGCGGAGCAGCTGTACCCAGGCTACTTCCATG	120		
Db	227	GGTCTGATGACACCTTTGCAGCCTACACACAGGAGCAGCTCTACCAAGCCATCTTCTATG	286		
QY	121	CTGTGGACCACTACCTTGGCGTTGCCTGACGTGTCACTGGGCGGATATCCCTGATGTCGGTG	180		
Db	287	CTGTGGACCACTACCTGATACTACTACCTGAGATATCCCTGGGCGGATATGCTATGTCGGTG	346		
QY	181	GTGGGGGTGACCCCTTGGAACCAATGGCTCAGGGCTTGCTCTCTGCCAGCGGTACTACCACC	240		
Db	347	GTGGGGGTGGGCCCTTGGGCCCAATGGATCAGCTTTGGCTCTCTGCCAGCGGTACTACCACC	406		
QY	241	GAGGCCACGTGGACCCGSCCAACGACACATTTGACATGATCCGATGGTGGTTACTGACT	300		
Db	407	GTGGCCATGTGGACCCAGCCCAATGATACCTTTGACATGATCCAAAGGTAGTCACTGACT	466		
QY	301	GCATCCAGGTGGATCCCGCCGAGCGGCCCTCCGCCGCCCGGACGACGATCTCACCCCTCT	360		
Db	467	GTATCCAGGTGGATCCCTCTGACAGACCCCTTGACATCCCGAGTGAGACTTGGACTTCT	526		
QY	361	TGGAAGCAGCTCCAGTTACAAGAACCTCAAGCTCAAAATCCACAAAGTGGTCAATGTCA	420		
Db	527	TGGATGGCAGCGCCAGTTACAAGAACCTCACTGAAATTCACAAAGTGATCAACGTCA	586		
QY	421	CCATCCACTTCCGGCTGAAGACCAATTAACCTCAGAGCCTCATCAATAATGAGATCCCGG	480		
Db	587	CCATCCACTTCCAGCTGAAGACCAATTAACCTGAGAGCCTCATCAATAATGAGATCCCTG	646		
QY	481	ACTGCTATACCTTCAGCGCTCTGATCACAGTTTGACAAACAAAGCACACAGTGGCGGATCC	540		
Db	647	ATTGTTACACCTTTCAGTATCCTGATCACATTTGACAAATAAAGCGCACAGTGGCGAATCC	706		
QY	541	CCATCAGCCTGGAGACCGGCCCCACATCCAGAGTGTAAAGCACCCCACTGTCTTCCAGC	600		
Db	707	CCATCCGCTGGAGACCAAGACCCACATCCAGAGTGCAACACCCCACTGTCTCCAGAC	766		
QY	601	ACGGAGACAACAGCTTCCGGCTCCTGTTTGACGTGGTGTCTATCCTCACCTGCTCCCTGT	660		
Db	767	ATGGAGACAACAGCTTCCGGCTTCTGTTTGATGTGGTGTATCCTCACCTGCTCCCTGT	826		
QY	661	CCTTCCTCCTCTCGCCCGCTCACTCCTTCGAGGCTTCTGCTGCAGAACGAGTTTGTGG	720		
Db	827	CCTTCCTGCTGTGCGCCCGCTCACTGCTCCGTCGCTTCTGCTGCAGAACGAGTTTGTG	886		
QY	721	GGTTCAATGTGGCGGACGGGGACGGGTCAATCAGCCTGTGGGAGCGGTGGAATTTGTCA	780		
Db	887	TATTCAATGTGGCGGCGCGGGTCCGGAAATCAGCCTCTGGGAACGGGTGGAGTTTGTCA	946		
QY	781	ATGGCTGTATACCTGCTCGTCAACGAGGATGTGCTCACCATCTCGGSCACCATCATGA	840		
Db	947	ATGGCTGTATACCTGCTCGTCAACGAGTGTGCTCACCATCTCGGSCACCATCATGA	1006		
QY	841	AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCCTCCTGGCA	900		
Db	1007	AGATTGGCATTGAGSCAAGAACCTAGCCAGTATGATGTCTGCAGTATTCTCTTGGTA	1066		
QY	901	CCTCGACGCTGCTGGTGGGTGGCGGTGATCCGCTACCTGACCTTCTTCCACAATACA	960		
Db	1067	CCTCCACTGCTGCTAGTCTGGTGGGTGCTATTCGCTACCTGACATTTTCCACAAGTACA	1126		
QY	961	ATATCCTCATCGCCACACTCGGGTGGCCCTGCCAGCGTCAATGCGTTCTGCTGTCGG	1020		
Db	1127	ACATCTTGATTGCCACGTTGCGAGTGGCACTGCCAGTGTCAATGCGTTTCTGCTGCTGTG	1186		

QY	1021	TGGCTGTCACTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGTGGGCCCTATCATG	108
Db	1187	TGGCTGTCACTACCTGGGCTATTGCTTCTGTGGCTGGATCGTGTGGGCCCTACCATG	1246
QY	1081	TGAAGTTCCGCTCACTCTCCA	1101
Db	1247	TGAAGTTCCGCTCGCTGTCCA	1267
RESULT 11			
AAS72274			
ID	AAS72274 standard; cDNA; 2092 BP.		
XX			
AC	AAS72274;		
XX			
DT	13-FEB-2002 (first entry)		
XX			
DE	DNA encoding novel human diagnostic protein #8078.		
XX			
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;		
KW	food supplement; medical imaging; diagnostic; genetic disorder; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200175067-A2.		
XX			
PD	11-OCT-2001.		
XX			
PF	30-MAR-2001; 2001WO-US08631.		
XX			
PR	31-MAR-2000; 2000US-0540217.		
PR	23-AUG-2000; 2000US-0649167.		
XX			
PA	(HYSE-) HYSEQ INC.		
XX			
PI	Drmanac RT, Liu C, Tang YT;		
XX			
DR	WPI; 2001-639362/73.		
DR	P-PSDB; ABG08087.		
XX			
PT	New isolated polynucleotide and encoded polypeptides, useful in		
PT	diagnostics, forensics, gene mapping, identification of mutations		
PT	responsible for genetic disorders or other traits and to assess		
PT	biodiversity -		
XX			
PS	Claim 1; SEQ ID No 8078; 103pp; English.		
XX			
CC	The invention relates to isolated polynucleotide (I) and		
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,		
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome		
CC	and gene mapping, and in recombinant production of (II). The		
CC	polynucleotides are also used in diagnostics as expressed sequence tags		
CC	for identifying expressed genes. (I) is useful in gene therapy techniques		
CC	to restore normal activity of (II) or to treat disease states involving		
CC	(II). (II) is useful for generating antibodies against it, detecting or		
CC	quantitating a polypeptide in tissue, as molecular weight markers and as		
CC	a food supplement. (II) and its binding partners are useful in medical		
CC	imaging of sites expressing (II). (I) and (II) are useful for treating		
CC	disorders involving aberrant protein expression or biological activity.		
CC	The polypeptide and polynucleotide sequences have applications in		
CC	diagnostics, forensics, gene mapping, identification of mutations		
CC	responsible for genetic disorders or other traits to assess biodiversity		
CC	and to produce other types of data and products dependent on DNA and		
CC	amino acid sequences. AAS64197-AAS94564 represent novel human		
CC	diagnostic coding sequences of the invention.		
CC	Note: The sequence data for this patent did not appear in the printed		
CC	specification, but was obtained in electronic format directly from WIPO		
CC	at ftp.wipo.int/pub/published_pct_sequences.		
XX			
SQ	Sequence 2092 BP; 386 A; 668 C; 605 G; 433 T; 0 other;		
Query Match 58.3%; Score 642.2; DB 23; Length 2092;			
Best Local Similarity 83.5%; Pred. No. 1.2e-135;			

Matches 914; Conservative 0; Mismatches 48; Indels 133; Gaps 11;	
Qy	1 CATTCGGGAAGAGAACACCATCGCCTTCGACACACCTCTTCCTGCTGGCTACTCGGACG 60
Db	
Qy	401 CATTCGGGAAGAGAACACCATCGCCTTCGACACACCTCTTCCTGCTGGCTACTCGGACG 460
Db	
Qy	61 GAGCGGATGACACCTTCGAGCCCTACACGGGGAGCAGCTGTACAGGCCATCTCCATG 120
Db	
Qy	461 GAGCGGATGACACCTTCGAGCCCTACACGGGGAGCAGCTGTACAGGCCATCTCCATG 520
Db	
Qy	121 CTGTGGACCACTACCTGGCGTTGCTGACGTGTCACTGGCGGATGCTGATGTCGCTG 180
Db	
Qy	521 CTGTGGACCACTACCTGGCGTTGCTGACGTGTCACTGGCGGATGCTGATGTCGCTG 577
Db	
Qy	181 GTGGGGTGACCTTTGGACCAATGGCTCAGGCTTGTCTCTGCGAGCGGTACTACACC 240
Db	
Qy	578 -TGCGTGTGCTGACGTGTCACTGGGC--GGCTTGTCTCTGCGAGCGGTACTACACC 634
Db	
Qy	241 GAGCCACGTGGACCCGGCCAAACGACACATTTGACATTCGATGCTGGTGTACTGACT 300
Db	
Qy	635 GAGCCACGTGGACCCGGCCAAACGACACATTTGACATTCGATGCTGGTGTACTGACT 694
Db	
Qy	301 GCATCCAGGTGATCCCGCGAGCGGCCCTCCCGCCCGGACGATCTCACCTCT 360
Db	
Qy	695 GCATCCAGGTGATCCCGCGAGCGGCCCTCCCGCCCGGACGATCTCACCTCT 754
Db	
Qy	361 TGGAAGCAGCTCCAGTTACAGAACCTCACGCTCAAAATTCACAA----- 406
Db	
Qy	755 TGGAAGCAGCTCCAGTTACAGAACCTCACGCTCAAAATTCACAAAGTACTGCCTGTCTA 814
Db	
Qy	407 ----- 406
Db	
Qy	815 CTCGAGGGGGCCAGGAGTCTAGCACGCTGGCAGGGGACGCTGGGCGCGGAGG 874
Db	
Qy	407 -----GCTGCTCAATGTCA 423
Db	
Qy	875 GACCCGAAGACGCCCTGACCTCACCCGAGCCTCTGCTGCTAGGCTGCTCAATGTCA 934
Db	
Qy	424 TCCACTTCCGGCTGAAGACCATTAACCTCCAGAGCCTCATCAATATGAGATCCCGGACT 483
Db	
Qy	935 TCCACTTCCGGCTGAAGACCATTAACCTCCAGAGCCTCATCAATATGAGATCCCGGACT 994
Db	
Qy	484 GCTATACCTTCAGCGTCTGATCACGTTTGACAAACAAAGCACACAGTGGCGGATCCCA 543
Db	
Qy	995 GCTATACCTTCAGCGTCTGATCACGTTTGACAAACAAAGCACACAGTGGCGGATCCCA 1054
Db	
Qy	544 TCAGCCTGGAGACCCAGGCCACATCCAGAGGTGAAGCACCCCGAGTCTTCCAGCAG 603
Db	
Qy	1055 TCAGCCTGGAGACCCAGGCCACATCCAGAGGTGAAGCACCCCGAGTCTTCCAGCAG 1114
Db	
Qy	604 G--AGACAACAGCTTCC--GGCTCTGTTTGACGTGGTGTCTATCTCACCTGCTCCCTGT 660
Db	
Qy	1115 GGAGGACAACAGCTTCCGGGCTCTGTTTGACGTGGTGTCTATCTCACCTGCTCCCTGT 1174
Db	
Qy	661 CCTTCTCTCTGCGCCCGCTCACTCTTTCGAGGTTCTGCTGAGAAC--GAGTTTGTG 719
Db	
Qy	1175 ACTTCTCTCTGAGCCCGCTCACTCTTTCGAGGTTCTGCTGAGAACAGAGTTTGTG 1234
Db	
Qy	720 GGGTTCTATGCGGGGAGCGGGGACGGGTCTATCAGCTGTGGAGCGGTGAATTTGTC 779
Db	
Qy	1235 GGGTTCTATGCGGGGAGCGGGGACGGGTCTATCAGCTGTGGAGCGGTGAATTTGTC 1294
Db	
Qy	780 AATGGCTGTATCATCTCTGCTTCGTCACAGCGATGTGC--TCACCATCTCGGGCACCA--TC 836
Db	
Qy	1295 AATGGCTGTATCATCTCTGCTTCGTCACAGCGATGTGCTTACCATCTTGGGCACCATTC 1354
Db	
Qy	837 ATGAAGATCGGCATCGAGGGCCAGAACTTGGGGA--GCTACGAG--TCTGCAGCATCTCTC 893
Db	
Qy	1355 ATGAAGATCGGCATCGAGGGCCAGAACTTGGGGAAGCTTACGACGTTTTCAGCATCTCTC 1414
Db	
Qy	894 CTGGGCACCTCGACCGTGTGTGGTGGGCGGTATCCGCTACCTGACCTTCTTCCAC 953
Db	
Qy	1415 CTGGGCACCTCGACCGTGTGTGGTGGGCGGTATCCGCTACCTGACCTTCTTCCAC 1474
Db	

Qy	954 AACTACAATATCTCTC 968
Db	
Qy	1475 AACTACAATTTCCGC 1489
Db	
RESULT 12	
ABL89699	
ID	ABL89699 standard; cDNA; 734 BP.
XX	ABL89699;
AC	
XX	
DT	24-MAY-2002 (first entry)
XX	
DE	Human polynucleotide SEQ ID NO 261.
XX	
KW	Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW	antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW	vulnerable; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW	cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW	neurological disease; infection; human; secreted protein; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200190304-A2.
XX	
PD	29-NOV-2001.
XX	
PF	18-MAY-2001; 2001WO-US16450.
XX	
PR	19-MAY-2000; 2000US-205515P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Birse CE, Rosen CA;
XX	
DR	WPI; 2002-122018/16.
DR	P-PSDB; ABB89290.
XX	
PT	Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT	prevention of neural, immune system, muscular, reproductive,
PT	gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT	disorders -
XX	
PS	Claim 4; SEQ ID NO 261; 2081pp + Sequence Listing; English.
XX	
CC	The invention relates to novel genes (ABL89449-ABL90853) and proteins
CC	(ABB89040-ABB90444) useful for preventing, treating or ameliorating
CC	medical conditions e.g. by protein or gene therapy. The genes are
CC	isolated from a range of human tissues disclosed in the specification.
CC	The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC	in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC	and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC	marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC	(b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC	haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC	disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC	colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC	(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC	epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC	and parasitic infections.
CC	Note: The sequence data for this patent did not form part of the
CC	printed specification, but was obtained in electronic format directly
CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 734 BP; 134 A; 229 C; 193 G; 167 T; 11 other;
Query Match 49.0%; Score 539.6; DB 24; Length 734;	
Best Local Similarity 91.1%; Pred. No. 1.5e-112;	
Matches 622; Conservative 4; Mismatches 4; Indels 53; Gaps 3;	
Qy	405 AAGCTGTCAATGTCCACCATCCACTTCCGGCTGAAGACCATTAACCTCCAGAGCTCATC 464
Db	

Db 1 AAGCTGGTCAATGTACACCATCCACTTCCGGGTGAAGACCAATTAACCTCCAGAGCCTCATC 60
QY 465 AATAATGAGATCCGGACTGCTATACCTTCAGCGTCTGTATCACGTTT-GACAACAAGC 523
Db 61 AATAATNAGATCCCGACTGCTATACCTTCAGCGTCTGTATCACGTTTGGACAACAAGC 120
QY 524 ACACAGTGGG-CGATCCCCCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGAAGC 582
Db 121 ACACAGTGGCGGATCCCCATCAGCACGGAGA----- 153
QY 583 ACCCCAGTGTCTCCAGACGGAGACAACAGCTTCCGGCTCCTGTTTGACGTGGTGTCA 642
Db 154 -----ACACAGCTTCCGGCTCCTGTTTGACGTGGTGTCA 189
QY 643 TCCTCACCTGCTCCCTGTCTCTCCTCTGCGCCCGCTCACTCCTTCGAGGCTTCCTGC 702
Db 190 TCCTCACCTGCTCCCTGTCTCTCCTCTGCGCCCGCTCACTCCTTCGCGGCTTCCTGC 249
QY 703 TGCAGAACGATTGTGGGTTTCATGTGGCGGCAGCGGACGGGTTCATCAGCCTGTGGG 762
Db 250 TGCAGAACGATTGTGGGTTTCATGTGGCGGCAGCGGACGGGTTCATCAGCCTGTGGG 309
QY 763 AGCGGCTGGAATTGTCAATGGTGGTATCATCTGCTCGTCACGAGCGATGTGCTACCA 822
Db 310 AGCGGCTGGAATTGTCAATGGTGGTATCATCTGCTCGTCACGAGCGATGTGCTACCA 369
QY 823 TCTCGGCACCATCATGAAGATCGGCATCGAGGCCAAGAACTGGCGAGCTACGAGTCT 882
Db 370 TCTCGGCACCATCATGAAGATCGGCATCGAGGCCAAGAACTGGCGAGCTACGAGTCT 429
QY 883 GCAGCATCCTCTGGGCACCTCGACGCTGCTGGTGTGGGTGGCGGTGATCCGCTACCTGA 942
Db 430 GCAGCATCCTCTGGGCACCTCGACGCTGCTGGTGTGGGTGGCGGTGATCCGCTACCTGA 489
QY 943 CTTTCTTCCAACTACAATATCCTCATCGCCACACTCGGGTGGCCCTGCCAGCGTCA 1002
Db 490 CTTTCTTCCAACTACAATATCCTCATCGCCACACTCGGGTGGCCCTGCCAGCGTCA 549
QY 1003 TCGCTTCTGCTGCTGCTGGTGTGCTATCTACCTGGGCTACTGCTTCTGTGGCTGATCG 1062
Db 550 TCGCTTCTGCTGCTGCTGGTGTGCTATCTAMCTGGGCTACTGCTTCTGTGGCTGATCG 609
QY 1063 TGCTGGGCGCCTATCATGTGAAG 1085
Db 610 TGCTGGGSCCTATCATGTKAAG 632

RESULT 13

AAS72273
ID AAS72273 standard; cDNA; 499 BP.
XX AC AAS72273;
XX DT 13-FEB-2002 (first entry)
XX DE DNA encoding novel human diagnostic protein #8077.
XX OS Homo sapiens.
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX

PI Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
DR P-PSDB; ABG08086.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 1; SEQ ID No 8077; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

Sequence 499 BP; 73 A; 158 C; 143 G; 125 T; 0 other;

Query Match 41.6%; Score 458; DB 23; Length 499;
Best Local Similarity 98.9%; Pred. No. 3.9e-94;
Matches 461; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 636 GTGTCATCTCACCTGCTCCTGTCTCCTTCTCCTCTGCGCCCGCTCACTCCTTCGAGGC 695
Db 6 GAGGGCATCTCACCTGCTCCTGCTCCTTCTCCTCTGCGCCCGCTCACTCCTTCGAGGC 65
QY 696 TTCCTGCTGCAGAACGAGTTTGTGGGTTTCATGTGGCGGCAGCGGGACGGTCAATCAGC 755
Db 66 TTGCTGCTGCAGAAATGAGTTTGTGGGTTTCATGTGGCGGCAGCGGGACGGTCAATCAGC 125
QY 756 CTGTGGGAGCGGCTGGAATTTGTCAATGGCTGGTACATCTGCTGCACACGCGATGTG 815
Db 126 CTGTGGGAGCGGCTGGAATTTGTCAATGGCTGGTACATCTGCTGCACACGCGATGTG 185
QY 816 CTCACCATCTCGGGCACCATCATGAAGATCGGCATCGAGGCCAAGAACTTGGCGAGCTAC 875
Db 186 CTCACCATCTCGGGCACCATCATGAAGATCGGCATCGAGGCCAAGAACTTGGCGAGCTAC 245
QY 876 GACGTCTGCAGCATCTCTCTGGGCACCTCGACCGTGTGGTGTGGGTGGCGGTGATCCGC 935
Db 246 GACGTCTGCAGCATCTCTCTGGGCACCTCGACCGTGTGGTGTGGGTGGCGGTGATCCGC 305
QY 936 TACCTGACCTTCTTCCAACTACAATATCCTCATCGCCACACTCGGGTGGCCCTGCC 995
Db 306 TACCTGACCTTCTTCCAACTACAATATCCTCATCGCCACACTCGGGTGGCCCTGCC 365
QY 996 AGCGTCATGGCTTCTGCTGCTGGTGTGCTATCTACCTGGGCTACTGCTTCTGTGGC 1055
Db 366 AGCGTCATGGCTTCTGCTGCTGGTGTGCTATCTACCTGGGCTACTGCTTCTGTGGC 425
QY 1056 TGGATCGTGTGGGCGCCTATCATGTGAAGTTCGCTCACTCTCCA 1101
Db 426 TGGATCGTGTGGGCGCCTATCATGTGAAGTTCGCTCACTCTCCA 471

CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 776 BP; 141 A; 243 C; 248 G; 144 T; 0 other;

Query Match 25.7%; Score 282.8; DB 23; Length 776;
Best Local Similarity 99.0%; Pred. No. 1.9e-54;
Matches 295; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCTGCTGGGCTACTCGGACG 60
Db |||||||
401 CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCTGCTGGGCTACTCGGACG 460
QY 61 GAGCGGATGACACCTTCGCAGCCTACACGGGGAGCAGCTGTACCAAGGCCATCTTCCATG 120
Db |||||||
461 GAGCGGATGACACCTTCGCAGCCTACACGGGGAGCAGCTGTACCAAGGCCATCTTCCATG 520
QY 121 CTGTGGACCACTACCTGGCGTTGCCCTGACGTGTCACTGGGCGGATATGCGTATGTCCGTG 180
Db |||||||
521 CTGTGGACCACTACCTGGCGTTGCCCTGACGTGTCACTGGGCGGATATGCGTATGTCCGTG 580
QY 181 GTGGGGGTGACCCCTTGGAACCAATGGCTCAGGCTTGCTCTCTGCCAGCGGTACTACCACC 240
Db |||||||
581 GTGGGGGTGACCCCTTGGAACCAATGGCTCAGGCTTGCTCTCTGCCAGCGGTACTACCACC 640
QY 241 GAGGCCACGTGGACCCGGCCAAACGACACATTGACATTGAT-CCGATGGTGGTTACTG 297
Db |||||||
641 GAGGCCACGTGGACCCGGCCAAACGACACATTGACATTGATCCCGATGGTGGTTACTG 698

Search completed: October 27, 2003, 12:34:25
Job time : 368.835 secs

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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:10:42 ; Search time 4411.07 Seconds
(without alignments)
10211.014 Million cell updates/sec

Title: US-09-851-494B-2_COPY_400_1500
Perfect score: 1101
Sequence: 1'cattccgggaagagacacc.....gaagttccgctcactctcca 1101

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_or:
22: em_ov:
23: em_pat:
24: em_ph:
25: em_pl:
26: em_ro:
27: em_sts:
28: em_un:
29: em_vi:
30: em_htg_hum:
31: em_htg_inv:
32: em_htg_other:
33: em_htg_mus:
34: em_htg_pln:
35: em_htg_rod:
36: em_htg_mam:
37: em_htg_vrt:
38: em_sy:
39: em_htgo_hum:
40: em_htgo_mus:
41: em_htgo_other:

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1101	100.0	1740	6	AX280021	AX280021 Sequence
2	1101	100.0	2004	9	AF249319	AF249319 Homo sapi
3	1101	100.0	2049	9	AK026102	AK026102 Homo sapi
4	1101	100.0	2051	9	AF287269	AF287269 Homo sapi
5	1101	100.0	2087	9	BC005149	BC005149 Homo sapi
6	1101	100.0	2095	6	AX280019	AX280019 Sequence
7	1099.4	99.9	2037	9	HSA293970	AJ293970 Homo sapi
8	1099.4	99.9	2052	6	AX083508	AX083508 Sequence
9	854.4	77.6	2272	9	HSA293659	AJ293659 Homo sapi
10	851.4	77.3	2003	10	AF302009	AF302009 Mus muscu
11	851.4	77.3	2039	10	BC005651	BC005651 Mus muscu
12	317.8	28.9	1662	10	AY083531	AY083531 Mus muscu
13	317.8	28.9	1712	10	AF475086	AF475086 Mus muscu
14	298.6	27.1	1900	9	AF475085	AF475085 Homo sapi
15	260.8	23.7	1762	6	BD156806	BD156806 Primer fo
16	260.8	23.7	1762	9	AK001868	AK001868 Homo sapi
17	239.8	21.8	1617	10	AY083532	AY083532 Mus muscu
18	239.8	21.8	2390	10	BC029847	BC029847 Mus muscu
19	239.8	21.8	2505	10	AF503575	AF503575 Mus muscu
20	198.2	18.0	1617	9	AY083533	AY083533 Homo sapi
21	188.8	17.1	2010	5	BC044140	BC044140 Danio rer
22	169	15.3	13270	9	AF287270	AF287270 Homo sapi
23	169	15.3	155645	2	AC021153	AC021153 Homo sapi
24	169	15.3	173126	9	AC008878	AC008878 Homo sapi
25	159.6	14.5	1351	9	AF305572S6	AF305577 Homo sapi
26	157	14.3	790	9	AF305572S3	AF305574 Homo sapi
27	137.4	12.5	233670	2	AC126740	AC126740 Rattus no
28	137.4	12.5	245259	2	AC120898	AC120898 Rattus no
29	135.8	12.3	200848	2	AC079544	AC079544 Mus muscu
30	131	11.9	2727	9	AK093948	AK093948 Homo sapi
31	119.6	10.9	3085	3	AY070709	AY070709 Drosophil
32	111	10.1	332	9	AF305572S4	AF305575 Homo sapi
33	103.8	9.4	579	9	AF305572S5	AF305576 Homo sapi
34	100.6	9.1	2403	9	AK094010	AK094010 Homo sapi
35	84.8	7.7	2264	9	AK095148	AK095148 Homo sapi
36	84.8	7.7	26904	2	AC017729	AC017729 Drosophil
37	84.8	7.7	150884	2	AC009382	AC009382 Drosophil
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39	84.8	7.7	289990	3	AE003516	AE003516 Drosophil
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41	79.6	7.2	156651	2	BX284638	BX284638 Danio rer
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45	77	7.0	165799	9	AL358789	AL358789 Human DNA

ALIGNMENTS

RESULT 1
AX280021
LOCUS AX280021 1740 bp
DEFINITION Sequence 3 from Patent WO0177331.
ACCESSION AX280021
VERSION AX280021.1 GI:16607475
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Curtis,R.A. and Silos-Santiago,I.
TITLE Human trp-like calcium channel protein-2 (tlcc-2)
JOURNAL Patent: WO 0177331-A 3 18-OCT-2001;

AX280021 linear DNA PAT 02-NOV-2001

MILLENIUM PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
1. .>1740
/note="unnamed protein product"
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/translation="MTAPAGPRGSETERLLTPNPGYGTQAGPSPAPPTPPEEEDLRRR
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BASE COUNT 319 a 578 c 475 g 368 t
ORIGIN

Query Match 100.0%; Score 1101; DB 6; Length 1740;
Best Local Similarity 100.0%; Pred. No. 9.7e-195;
Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTCCGGGAAGAGAACACCATCGCCTTCGACACCTCTTCCGCTGGGCTACTCGGACG 60
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275 CATTCCGGGAAGAGAACACCATCGCCTTCGACACCTCTTCCGCTGGGCTACTCGGACG 334

QY 61 GAGCGGATGACACCTTCGAGCCTACACGGGGAGCAGCTGTACAGGCCATCTTCCATG 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
335 GAGCGGATGACACCTTCGAGCCTACACGGGGAGCAGCTGTACAGGCCATCTTCCATG 394

QY 121 CTGTGGACCGATCTGGCGTTGCCTGACGTGTCACTGGCGCGTATCGGTATGTCCTGTG 180
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395 CTGTGGACCGATCTGGCGTTGCCTGACGTGTCACTGGCGCGTATGCGTATGTCCTGTG 454

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455 GTGGGGGTGACCCCTTGGACCAATGGCTCAGGCTTGCTCTCTGCGCAGCGGTACTACACC 514

QY 241 GAGGCCACGTGGACCCCGCCAAACGACACATTGTGACATTGATCCGATGGTGTACTGACT 300
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QY 301 GCATCCAGGTGATCCCCCGGAGCGGCCCTCCGCCCCCGGCGGCTCCGCCCCCGGCGATCT 360
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575 GCATCCAGGTGATCCCCCGGAGCGGCCCTCCGCCCCCGGCGGCGATCTCACCCTCT 634

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QY 421 CCATCCACTTCCGCTGAAGACCATTAACCTCCAGAGCCTCATCAATAATGAGATCCCGG 480
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QY 481 ACTGCTATACCTTCAGCGTCTCTGATCAGCTTTGACAACAAAGCACACAGTGGCGGATCC 540
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QY 541 CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGTAAAGACCCAGTGTCTTCCAGC 600
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995 GGTTCATGTGGCGGACGCGGACGGGTTCATCAGCCTGTGGGAGCGGTGGAAATTTGTCA 1054

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1055 ATGGCTGTACATCCTGCTCGTCACCAGCGATGTGTCACCATCTCGGGCACCATCATGA 1114

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1355 TGAAGTTCGGCTCACTCTCCA 1375

RESULT 2
AF249319 2004 bp mRNA linear PRI 22-SEP-2000
LOCUS Homo sapiens mucolipidosis type IV protein (MLIV) mRNA, complete
DEFINITION
ACCESSION AF249319
VERSION AF249319.1 GI:9971787
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2004)
AUTHORS Bargal,R., Avidan,N., Ben-Asher,E., Olender,Z., Zeigler,M.,
Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.
TITLE Identification of the gene causing mucolipidosis type IV
JOURNAL Nat. Genet. 26 (1), 118-123 (2000)
MEDLINE 20428196
PUBMED 10973263
REFERENCE 2 (bases 1 to 2004)
AUTHORS Bargal,R., Avidan,N., Ben-Asher,E., Olender,Z., Zeigler,M.,
Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.
TITLE Direct Submision
JOURNAL Submitted (26-MAR-2000) Molecular Genetics, The Weizmann Institute
of Science, P. O. Box 26, Rehovot 76100, Israel
FEATURES
source Location/Qualifiers
1. .2004
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1. .2004
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BASE COUNT 352 a 665 c 568 g 419 t
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Query Match 100.0%; Score 1101; DB 9; Length 2004;
Best Local Similarity 100.0%; Pred. No. 9.6e-195;
Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 959 ACGGAGACAACAGCTTCCGGCTCCTGTTTGACGTGGTGGTATCCTCACCTGCTCCCTGT 1018
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QY 1379 TGGCTGTCATCTACCTGGGTACTGCTTCTGTGGTGGATCGTGTGGGCCCTCATCATG 1438
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Db |||||
QY 1439 TGAAGTTCGGCTCACTCTCCA 1459
Db |||||

RESULT 3
AK026102
LOCUS 2049 bp mRNA linear PRI 29-SEP-2000
DEFINITION Homo sapiens cDNA: FLJ22449 fis, clone HRC09609.
ACCESSION AK026102
VERSION AK026102.1 GI:10438843
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (sites)
AUTHORS Kawabata,A., Hikiiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished
REFERENCE 2 (bases 1 to 2049)
AUTHORS Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing; Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing; Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).

FEATURES
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CDS

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ORIGIN					
Query Match		100.0%; Score 1101; DB 9; Length 2049;			
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Matches 1101; Conservative		0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	CATTCCGGGAGAGAAACACCATCGCCTTCGGACACCTCTTCCCTGCTGGGTACTCGGACG	60		
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QY	661	CCTTCCTCCTCTCGGCCCGCTCACTCCTTCGAGGCTTCTGCTGCAGAACGAGTTTGTGG	720		
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QY	841	AGATCGGCATCGAGGCCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCCTCTGGGCA	900		
Db	1210	AGATCGGCATCGAGGCCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCCTCTGGGCA	1269		

QY	901	CCTGACCGCTGCTGGTGGGTGGCGGTGATCCGCTACTGACCTTCTTCCACAACACTACA	960
Db	1270	CCTGACCGCTGCTGGTGGGTGGCGGTGATCCGCTACTGACCTTCTTCCACAACACTACA	1329
QY	961	ATAATCCTCATCGCCACACTGCGGTGGCCCTGCCAGCGTCATGCGCTTCTGCTGCTCGG	1020
Db	1330	ATAATCCTCATCGCCACACTGCGGTGGCCCTGCCAGCGTCATGCGCTTCTGCTGCTCGG	1389
QY	1021	TGGCTGTCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTCTGGGGCCCTATCATG	1080
Db	1390	TGGCTGTCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTCTGGGGCCCTATCATG	1449
QY	1081	TGAAGTTCGGCTCACTCTCCA	1101
Db	1450	TGAAGTTCGGCTCACTCTCCA	1470
RESULT 4			
AF287269			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
gene			
CDS			
BASE COUNT			
ORIGIN			
Query Match			

Best Local Similarity 100.0%; Pred. No. 9.6e-195;			
Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTCTCTGCTGGGCTACTCGGACG	60
DB	400	CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTCTCTGCTGGGCTACTCGGACG	459
QY	61	GAGCGGTACACCTTCGACGCTTACACGCGGGAGCAGCTGTACAGGCCATCTTCATG	120
DB	460	GAGCGGTACACCTTCGACGCTTACACGCGGGAGCAGCTGTACAGGCCATCTTCATG	519
QY	121	CTGTGGACCACTGCTGGCTTGCCTGACGTGTACCTGGGCGGTATGCGTATGTCGTG	180
DB	520	CTGTGGACCACTGCTGGCTTGCCTGACGTGTACCTGGGCGGTATGCGTATGTCGTG	579
QY	181	GTGGGGGTGACCTTCGACCAATGGCTCAGGGCTTGTCTCTGCGCAGCGGTACTACACC	240
DB	580	GTGGGGGTGACCTTCGACCAATGGCTCAGGGCTTGTCTCTGCGCAGCGGTACTACACC	639
QY	241	GAGGCCACGTGGACCCCGCCAAACGACACATTTGACATTTGATCCGATGGTGTACTGACT	300
DB	640	GAGGCCACGTGGACCCCGCCAAACGACACATTTGACATTTGATCCGATGGTGTACTGACT	699
QY	301	GCATCCAGGTGATCCCGCCCGGAGCGGCCCTCCGCCCCCGCCAGCGATCTCACCCCTCT	360
DB	700	GCATCCAGGTGATCCCGCCCGGAGCGGCCCTCCGCCCCCGCCAGCGATCTCACCCCTCT	759
QY	361	TGGAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAATTCACAAAGCTGGTCAATGTCA	420
DB	760	TGGAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAATTCACAAAGCTGGTCAATGTCA	819
QY	421	CCATCCACTTCCGGGTGAAGACCATTAACCTCCAGAGCCTCATCAATAATGAGATCCCGG	480
DB	820	CCATCCACTTCCGGGTGAAGACCATTAACCTCCAGAGCCTCATCAATAATGAGATCCCGG	879
QY	481	ACTGCTATACCTTCAGCGTCTCTGATCAGTTTGACAACAAAGCAGAGTGGCGGATCC	540
DB	880	ACTGCTATACCTTCAGCGTCTCTGATCAGTTTGACAACAAAGCAGAGTGGCGGATCC	939
QY	541	CCATCAGCCTGGAGACCCAGGCCACATCCAGAGTGTAAAGCACCCAGTGTCTTCCAGC	600
DB	940	CCATCAGCCTGGAGACCCAGGCCACATCCAGAGTGTAAAGCACCCAGTGTCTTCCAGC	999
QY	601	ACGGAGACAAACAGTTCCGGCTCCTGTTTGACGTGGTGTATCCTCAGCTGCTCCCTGT	660
DB	1000	ACGGAGACAAACAGTTCCGGCTCCTGTTTGACGTGGTGTATCCTCAGCTGCTCCCTGT	1059
QY	661	CCTTCCTCCTCTGCGCCCGCTCACTCCTTCGAGGTTCTCTGCTGCAGAACGATTTGTGG	720
DB	1060	CCTTCCTCCTCTGCGCCCGCTCACTCCTTCGAGGTTCTCTGCTGCAGAACGATTTGTGG	1119
QY	721	GGTTTCATGTGGCGGACGCGGGACGGGTATCAGCTGTGGAGCGGTGGAATTTGTCA	780
DB	1120	GGTTTCATGTGGCGGACGCGGGACGGGTATCAGCTGTGGAGCGGTGGAATTTGTCA	1179
QY	781	ATGGCTGGTACATCCTGCTCGTCCAGCGATGTGCTCACCATCTCGGCGACCATCATGA	840
DB	1180	ATGGCTGGTACATCCTGCTCGTCCAGCGATGTGCTCACCATCTCGGCGACCATCATGA	1239
QY	841	AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCGACATCTCTCTGGGCA	900
DB	1240	AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCGACATCTCTCTGGGCA	1299
QY	901	CCTCGACGCTGCTGGTGTGGGTGGCGGTGATCCGCTACCTGACCTTCTTCCAACTACA	960
DB	1300	CCTCGACGCTGCTGGTGTGGGTGGCGGTGATCCGCTACCTGACCTTCTTCCAACTACA	1359
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DB	1360	ATATCCTCATCGCCACACTCGCGGTGGCCCTGCCCCAGCGTATCGGCTTCTGCTGCTGG	1419
QY	1021	TGGCTGTATCTACCTGGGCTACTGCTTCTGTGGCTGATCGTCTGGGCGCCCTATCATG	1080

Db	1420	TGGCTGTCTATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGTGGGCGCCCTATCATG	1479
QY	1081	TGAAGTTCCGCTCACTCTCCA	1101
Db	1480	TGAAGTTCCGCTCACTCTCCA	1500
RESULT 5			
BC005149	2087 bp mRNA linear PRI 12-JUL-2001		
LOCUS	Homo sapiens, mucolipin 1, clone MGC:3287 IMAGE:3507836, mRNA, complete cds.		
ACCESSION	BC005149		
VERSION	BC005149.1 GI:13477346		
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 2087)		
AUTHORS	Straussberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (26-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbio.org contact: amadan@systemsbiology.org Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Kettelman and Anuradha Madan		
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 7 Row: c.Column: 22 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9844923.		
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	/db_xref="taxon:9606"		
	/clone="MGC:3287 IMAGE:3507836"		
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	/lab_host="DH10B-R"		
	/note="Vector: pOTB7"		
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	/protein_id="AAH05149.1"		
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BASE COUNT	391 a	677 c	592 g 427 t
ORIGIN			

Query Match		100.0%;	Score 1101;	DB 9;	Length 2087;
Best Local Similarity		100.0%;	Pred. No. 9.6e-195;		
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QY	1	CATTCCGGGAAGAGAACACCATCGCCTTCGACACCTCTTCCCTGCTGGCTACTCGGACG	60		
Db	407	CATTCCGGGAAGAGAACACCATCGCCTTCGACACCTCTTCCCTGCTGGCTACTCGGACG	466		
QY	61	GAGCGGATGACACCTTCGCAGCCTACACGGGGAGCAGCTGTACAGGCCATCTTCCATG	120		
Db	467	GAGCGGATGACACCTTCGCAGCCTACACGGGGAGCAGCTGTACAGGCCATCTTCCATG	526		
QY	121	CTGTGGACCACTGCTGGCGTTGCCTGACGTGTCACTGGGCCGGTATGCGTATGTCGGTG	180		
Db	527	CTGTGGACCACTGCTGGCGTTGCCTGACGTGTCACTGGGCCGGTATGCGTATGTCGGTG	586		
QY	181	GTGGGGGTGACCTTGGACCAATGGCTCAGGCTTGCTCTCTGCCAGCGGTACTACCACC	240		
Db	587	GTGGGGGTGACCTTGGACCAATGGCTCAGGCTTGCTCTCTGCCAGCGGTACTACCACC	646		
QY	241	GAGGCCACGTGGACCCGGCCAAACGACACATTTGACATTGATCCGATGGTGTACTGACT	300		
Db	647	GAGGCCACGTGGACCCGGCCAAACGACACATTTGACATTGATCCGATGGTGTACTGACT	706		
QY	301	GCATCCAGGTGGATCCCGCCCGGAGCGGCCCTCCGCCCCCAGCGAGCATCTCACCCCTCT	360		
Db	707	GCATCCAGGTGGATCCCGCCCGGAGCGGCCCTCCGCCCCCAGCGAGCATCTCACCCCTCT	766		
QY	361	TGGAAGCAGCTCCAGTTACAAGAACCTCACGCTCAAATTCACAAAGTGGTCAATGTCA	420		
Db	767	TGGAAGCAGCTCCAGTTACAAGAACCTCACGCTCAAATTCACAAAGTGGTCAATGTCA	826		
QY	421	CCATCCACTTCCGGCTGAAGACCATTAACTCCAGAGCCTCATCAATAATGAGATCCCGG	480		
Db	827	CCATCCACTTCCGGCTGAAGACCATTAACTCCAGAGCCTCATCAATAATGAGATCCCGG	886		
QY	481	ACTGCTATACCTTCAGCGTCTGATCACGTTTGACAAACAAAGCACACAGTGGCGGATCC	540		
Db	887	ACTGCTATACCTTCAGCGTCTGATCACGTTTGACAAACAAAGCACACAGTGGCGGATCC	946		
QY	541	CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGTAAAGCACCCCAAGTGTCTTCCAGC	600		
Db	947	CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGTAAAGCACCCCAAGTGTCTTCCAGC	1006		
QY	601	ACGGAGACAAACAGCTTCCGGCTCCTGTTTGACGCTGGTGGTCACTCCTCACTGCTCCCTGT	660		
Db	1007	ACGGAGACAAACAGCTTCCGGCTCCTGTTTGACGCTGGTGGTCACTCCTCACTGCTCCCTGT	1066		
QY	661	CCTTCCTCCTCTGCGCCCGCTCACTCCTTCGAGGCTCCTGCTGCAGACGAGTTTGTGG	720		
Db	1067	CCTTCCTCCTCTGCGCCCGCTCACTCCTTCGAGGCTCCTGCTGCAGACGAGTTTGTGG	1126		
QY	721	GSTTCATGTGGCGGACGGGGACGGGTCACTCAGCTGTGGAGCGGCTGGAATTTGTCA	780		
Db	1127	GSTTCATGTGGCGGACGGGGACGGGTCACTCAGCTGTGGAGCGGCTGGAATTTGTCA	1186		
QY	781	ATGCTGGTACATCCTCTGCTCCTCACCGCATGTGTCAACCATCTCGGGCACCATCATGA	840		
Db	1187	ATGCTGGTACATCCTCTGCTCCTCACCGCATGTGTCAACCATCTCGGGCACCATCATGA	1246		
QY	841	AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACAGCTGTGACGATCCTCCTGGGCA	900		
Db	1247	AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACAGCTGTGACGATCCTCCTGGGCA	1306		
QY	901	CCTCGACGCTGCTGGTGTGGTGGGCGTGTATCCGCTACCTGACCTTCTTCCAACTACA	960		
Db	1307	CCTCGACGCTGCTGGTGTGGTGGGCGTGTATCCGCTACCTGACCTTCTTCCAACTACA	1366		
QY	961	ATATCCTCATCGCCACACTGCGGCTGGCCCTGCCACGCTCATGCGCTTCTGCTGTGCG	1020		
Db	1367	ATATCCTCATCGCCACACTGCGGCTGGCCCTGCCACGCTCATGCGCTTCTGCTGTGCG	1426		
QY	1021	TGGCTGTCACTACCTGGGGTACTGCTTCTGTGGCTGGATCGTGTGGGGCCCTATCATG	1080		

Db	1427	TGGCTGTCACTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGTGGGCCCTATCATG	1486		
QY	1081	TGAAGTTCGGCTCACTCTCCA	1101		
Db	1487	TGAAGTTCGGCTCACTCTCCA	1507		
RESULT 6					
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LOCUS					
DEFINITION	AX280019				
ACCESSION	AX280019				
VERSION	AX280019.1				
KEYWORDS	GI:16607473				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1				
AUTHORS	Curtis, R.A. and Silos-Santiago, I.				
TITLE	Human trp-like calcium channel protein-2 (tlcc-2)				
JOURNAL	Patent: WO 0177331-A 1 18-OCT-2001; MILLENIUM PHARMACEUTICALS, INC. (US)				
FEATURES	Location/Qualifiers				
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BASE COUNT	388 a	682 c	594 g	431 t	
ORIGIN					
Query Match	100.0%; Score 1101; DB 6; Length 2095;				
Best Local Similarity	100.0%; Pred. No. 9.6e-195;				
Matches 1101; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
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Db	415	CATTCCGGGAAGAGAACACCATCGCCTTCGACACCTCTTCCCTGCTGGCTACTCGGACG	474		
QY	61	GAGCGGATGACACCTTCGCAGCCTACACGGGGAGCAGCTGTACAGGCCATCTTCCATG	120		
Db	475	GAGCGGATGACACCTTCGCAGCCTACACGGGGAGCAGCTGTACAGGCCATCTTCCATG	534		
QY	121	CTGTGGACCACTGCTGGCGTTGCCTGACGTGTCACTGGGCCGGTATGCGTATGTCGGTG	180		
Db	535	CTGTGGACCACTGCTGGCGTTGCCTGACGTGTCACTGGGCCGGTATGCGTATGTCGGTG	594		
QY	181	GTGGGGGTGACCCCTTGACCAATGGCTCAGGGCTTGTCTCTGCGACGGGTACTACCACC	240		
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Db	655	GAGGCCACGTGGACCCGGCCAAACGACACATTTGACATTGATCCGATGGTGTACTGACT	714		
QY	301	GCATCCAGGTGGATCCCGCGGAGCGGCCCTCCGCCCCCAGCGACGATCTCACCCCTCT	360		

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Db	775	TGGAAGCAGCTCCAGTTACAAGAACCTTCAGCTCAAATTCACAAGCTGGTCAATGTCA	834
QY	421	CCATCCACTTCCGGCTGAAGACCAATTAACCTCCAGAGCCTCATCAATAATGAGATCCCGG	480
Db	835	CCATCCACTTCCGGCTGAAGACCAATTAACCTCCAGAGCCTCATCAATAATGAGATCCCGG	894
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QY	541	CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGTAAAGACCCAGTGTCTTCCAGC	600
Db	955	CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGTAAAGACCCAGTGTCTTCCAGC	1014
QY	601	ACGGAGACAAACAGCTTCCGGCTCCTGTTGACGTGGTGTATCCTCACCTGCTCCCTGT	660
Db	1015	ACGGAGACAAACAGCTTCCGGCTCCTGTTGACGTGGTGTATCCTCACCTGCTCCCTGT	1074
QY	661	CCTTCCTCCTCTGCGCCGCTCACTCCTTCGAGGCTTCCCTGCTGAGAACGAGTTTGTG	720
Db	1075	CCTTCCTCCTCTGCGCCGCTCACTCCTTCGAGGCTTCCCTGCTGAGAACGAGTTTGTG	1134
QY	721	GGTTTCATGTGGCGGACGGGGACGGGTATCAGCCTGTGGGAGCGGCTGGAATTTGTCA	780
Db	1135	GGTTTCATGTGGCGGACGGGGACGGGTATCAGCCTGTGGGAGCGGCTGGAATTTGTCA	1194
QY	781	ATGGCTGGTACATCCTGTCTGTCACCAAGCGATGTGCTCACCATCTCGGGCACCATATGA	840
Db	1195	ATGGCTGGTACATCCTGTCTGTCACCAAGCGATGTGCTCACCATCTCGGGCACCATATGA	1254
QY	841	AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCCTCCTGGGCA	900
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QY	961	ATATCCTCATCGCCACACTGCGGGTGGCCCTGCCAGCGTCAATGCGCTTCTGCTGCTGG	1020
Db	1375	ATATCCTCATCGCCACACTGCGGGTGGCCCTGCCAGCGTCAATGCGCTTCTGCTGCTGG	1434
QY	1021	TGGCTGTATCTACCTGGGCTACTGCTTCTGTGGTGGATCGTGTGGGGCCCTATCATG	1080
Db	1435	TGGCTGTATCTACCTGGGCTACTGCTTCTGTGGTGGATCGTGTGGGGCCCTATCATG	1494
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Db	1495	TGAAGTTCGGCTCACTCTCCA	1515

RESULT 7
HSA293970
LOCUS HSA293970 2037 bp mRNA linear PRI 09-NOV-2000
DEFINITION Homo sapiens mRNA for mucolipidin (ML4 gene).
ACCESSION AJ293970
VERSION AJ293970.1 GI:10129689
KEYWORDS ML4 gene; mucolipidin.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bassi,M.T., Manzoni,M., Monti,E., Pizzo,M.T., Ballabio,A. and Borsani,G.
TITLE Cloning of the gene encoding a novel integral membrane protein, mucolipidin-and identification of the two major founder mutations causing mucolipidosis type IV

JOURNAL	Am. J. Hum. Genet. 67 (5), 1110-1120 (2000)
MEDLINE	20489855
PUBMED	11013137
REFERENCE	2 (bases 1 to 2037)
AUTHORS	Borsani,G.
TITLE	Direct Submision
JOURNAL	Submitted (08-SEP-2000) Borsani G., Tigem, Via Olgettina 58, Milano, ITALY
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QY	181 GTGGGGGTGACCCCTTGACCAATGGCTCAGGCTTGCTCTCTGCCAGCGGTACTACCACC 240
Db	535 GTGGGGGTGACCCCTTGACCAATGGCTCAGGCTTGCTCTCTGCCAGCGGTACTACCACC 594
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QY	301 GCATCCAGGTGGATCCCCCGAGCGGCCCTCCCTCCGCCCCCCCAGCGACGATCTCACCCCTCT 360
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Db	775 CCATCCACTTCCGGGTGAAGACCATTAACCTCCAGAGCCTCATCAATAATGAGATCCCGG 834

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QY 601 ACGGAGACAAACAGCTTCCGGCTCCTGTTTGACGTGGTGGTCACTCCTCACCTGCTCCCTGT 660
Db |||||||
QY 955 ACGGAGACAAACAGCTTCCGGCTCCTGTTTGACGTGGTGGTCACTCCTCACCTGCTCCCTGT 1014
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RESULT 8
AX083508
LOCUS AX083508
DEFINITION Sequence 50 from Patent WO0112662.
ACCESSION AX083508
VERSION AX083508.1 GI:13185318
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Lal,P., Yue,H., Tang,Y.T., Bandman,O., Burford,N., Azimzai,Y.,
Baughn,M.R., Lu,D.A. and Patterson,C.
TITLE Membrane associated proteins
JOURNAL Patent: WO 0112662-A 50 22-FEB-2001;
Incyte Genomics, Inc. (US)
FEATURES
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Query Match 99.9%; Score 1099.4; DB 6; Length 2052;

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RESULT 9

HSA293659

LOCUS HSA293659 2272 bp mRNA linear PRI 09-NOV-2000

DEFINITION Homo sapiens mRNA for mucolipidin, short form (ML4 gene).

ACCESSION AJ293659

VERSION AJ293659.1 GI:10045134

KEYWORDS alternative splicing; ML4 gene; mucolipidin.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1

AUTHORS Bassi,M.T., Manzoni,M., Monti,E., Pizzo,M.T., Ballabio,A. and Borsani,G.

TITLE Cloning of the gene encoding a novel integral membrane protein, mucolipidin-and identification of the two major founder mutations causing mucopolipidosis type IV

JOURNAL Am. J. Hum. Genet. 67 (5), 1110-1120 (2000)

MEDLINE 20489855

PUBMED 11013137

REFERENCE 2 (bases 1 to 2272)

AUTHORS Borsani,G.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-2000) Borsani G., Telethon Institute of Genetics and Medicine - TIGEM, Via Olgettina 58, 20132 Milano, ITALY

REMARK Revised by author

FEATURES

Location/Qualifiers

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421..2058

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ORIGIN

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Best Local Similarity 82.3%; Pred. No. 6.6e-149;

Matches 1100; Conservative 0; Mismatches 1; Indels 235; Gaps 1;

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Db 475 CTGTGGACCACTACCTGGCGTTGCCCTGACGTGTCACTGGCGGATGCGTATGTCCGTG 534

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Qy 407 -----GCTGTCAATGTCAACCATC 425

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QY	1026	GTCATCTACCTGGGCTACTGCTTCTGTGGTGGATCGTGTGGGGCCCTATCATGTGAAG	1085
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DEFINITION	Mus musculus mucolipin-1 (Mcoln1) mRNA, complete cds.		
ACCESSION	AF302009		
VERSION	AF302009.1	GI:18086903	
KEYWORDS			
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 2003)		
AUTHORS	Falardeau, J.L., Kennedy, J.C., Acerno, J.S., Sun, M., Stahl, S., Goldin, E. and Sclaughaupt, S.A.		
TITLE	Cloning and characterization of the mouse Mcoln1 gene		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 2003)		
AUTHORS	Falardeau, J.L., Kennedy, J.C., Acerno, J.S., Sun, M., Stahl, S., Goldin, E. and Sclaughaupt, S.A.		
TITLE	Direct Submission		
JOURNAL	Submitted (30-AUG-2000) Molecular Neurogenetics, Harvard Institute of Human Genetics, 77 Ave. Louis Pasteur, Boston, MA 02115, USA		
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QY	661	CCTTCCTCTCTGCGCCCGTCACTCCTTCGAGGCTTCTGCTGCAGAACGAGTTTGTGG	720
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QY	901	CCTCGACGCTGTGGTGGGTGGCGTGATCCGCTACCTGACCTTCTTCCACAACATA	960
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QY	961	ATATCCTCATCGCCACACTGCGGGTGGCCCTGCCAGCGTCATCGGCTTCTGCTGCTGG	1020
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Db	1430	TGAAGTTCGGCTCGCTGTCCA	1450
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BC005651 BC005651 2039 bp mRNA linear ROD 16-APR-2003
Mus musculus mucolipin 1, mRNA (cDNA clone MGC:7172 IMAGE:3257440),
complete cds.
ACCESSION BC005651
VERSION BC005651.1 GI:13542918
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2039)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,P.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 2039)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (02-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 6 Row: c Column: 16
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Similarity but not identity to protein.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
/strain="NMRI"
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gross tissue."

gene

CDS

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BASE COUNT 447 a 582 c 533 g 477 t
ORIGIN
Query Match 77.3%; Score 851.4; DB 10; Length 2039;
Best Local Similarity 85.8%; Pred. No. 2.4e-148;
Matches 945; Conservative 0; Mismatches 156; Indels 0; Gaps 0;
QY 1 CATTCCGGGAAGAGAACACCATCGCCTTCGGACACCTCTTCTGCTGGGTACTCGGACG 60
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DB 353 CATTCCGGGAAGAGAACACCATTCGCTTCCGACATCTCTTCTGCTGGGTACTCTGATG 412
QY 61 GAGCGGATGACACCTTCGCAGCCTACACGGGGAGGAGCAGCTGTACCAGGCCATCTTCCATG 120
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DB 413 GGTCTGATGACACCTTTGCAGCCTACACAGGAGCAGCTCTACCAAGCCATCTTCTATG 472
QY 121 CTGTGGACCAAGTACCTGGCGTTGCCCTGACGTGTCACTGGGCCGGTATGCCGTATGCCGTG 180
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DB 473 CTGTGGACCAAGTACCTGATACCTACCTGAGATATCCCTGGGCCGGTATGCCGTATGCCGTG 532
QY 181 GTGGGGGTGACCCCTTGACCAATGGCTCAGGGCTTGCTCTCTGCGCAGCGGTACTACCACC 240
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DB 593 GTGGCCATGTGGACCCAGCCCAATGATACCTTTGACATTTGATCCAAAGGTTAGTCACTGACT 652
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DB 713 TGGATGGCAGCGCCAGTTACAAGAACCTCAGCTGAAATTTCCACAAGCTGATCAACGTCA 772
QY 421 CCATCCACTTCCGGCTGAAGACCATTAACCTCCAGAGCCTCATCAATAATGAGATCCCGG 480
DB |||||
DB 773 CCATCCACTTCCAGCTGAAGACCAATTAACCTGCAGAGCCTCATCAACAATGAGATCCCTG 832
QY 481 ACTGCTATACCTTCAGCGTCTCTGATCAGCTTTGACAACAAAGCACACAGTGGCGGATCC 540
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DB 833 ATTGTTACACCTTCAGTATCCTGATCAGATTTGACAATAAAGCGCAGAGTGGCGGAATCC 892
QY 541 CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGTAAAGCACCCAGTGTCTTCCAGC 600
DB |||||
DB 893 CCATCCGCTGGAGACCAAGACCCACATCCAGGAGTGTCAAACACCCAGTGTCTCCAGAC 952
QY 601 ACGGAGACAACAGCTTCCGGCTCCTGTTGACGTTGGTGGTTCATCTCACCTGCTCCCTGT 660

Db 953 ATGGAGACAAACAGCTTCGGGCTTCTGTTTGATGGTGGTTATCCTCACCTGCTCCCTGT 1012
QY 661 CTTTCTCTCTGCGCGCTCACTCCTTCGAGGTTCTGCTGCAGACGAGTTTGTGG 720
Db 1013 CTTTCTCTGCTGCGCGCGCTCACTGCTCCGCTGCTCCTGCTGCAGACGAGTTTGTG 1072
QY 721 GGTTCATGTGGCGGCAGCGGGGACGGGTTCATCAGCCTGTGGGAGCGGCTGGAATTGTCA 780
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QY 841 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGTCTGCAGCATCCTCTCTGGGCA 900
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QY 1021 TGGCTGTCTATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGTGGGCGCCTATCATG 1080
Db 1373 TGGCTGTCTATCTACCTGGGCTATTGCTTCTGTGGCTGGATCGTGTCTAGGCGCCTACCATG 1432
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Db 1433 TGAAGTTCGGCTCGCTGTCCA 1453

RESULT 12
AY083531
LOCUS AY083531 1662 bp mRNA linear ROD 13-NOV-2002
DEFINITION Mus musculus mucolipin 3 (Mcoln3) mRNA, complete cds.
ACCESSION AY083531
VERSION AY083531.1 GI:24417796
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1662)
AUTHORS Di Palma,F., Belyantseva,I.A., Kim,H.J., Vogt,T.F., Kachar,B. and Noben-Trauth,K.
TITLE Mutations in Mcoln3 associated with deafness and pigmentation defects in varitint-waddler (Va) mice
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (23), 14994-14999 (2002)
PUBMED 12403827
REFERENCE 2 (bases 1 to 1662)
AUTHORS Di Palma,F. and Noben-Trauth,K.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-2002) National Institute on Deafness and Other Communication Disorders, National Institutes of Health, 5 Research Court, Rockville, MD 20850, USA
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BASE COUNT 445 a 405 c 383 g 429 t
ORIGIN
Query Match 28.9%; Score 317.8; DB 10; Length 1662;
Best Local Similarity 58.1%; Pred. No. 3.8e-49;
Matches 643; Conservative 0; Mismatches 422; Indels 42; Gaps 3;
QY 1 CATTCCGGGAAGAGAACACCATCGCCTTCCGACACCTCTTCTGCTGGGCTACTCGGACG 60
Db 266 CTTTCAAAGAGAGAAACACTATAGCCTTCAAACACCTCTTCTTAAAGGGCTACATGGATC 325
QY 61 GAGCGGATGACACCTTCGCAGCCTACACGGGGGAGCAGCTGTACCAGGCCATCTTCCATG 120
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Db 650 AGCTCCAGTTTAAGCTCAAAGCCATCAATCTGCAGACAGTTCCGACACCAAGGAGCTTCCCTG 709
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Db 710 ACTGTTACGACTTACGCTGACTATAACATTCGACAACAAGGCTCACAGTGAAGAATCA 769
QY 541 CCATCAGCCTGGAGACCCAGGCCACATCCAGGAGTGTAAAGCAACCCAGTGTCTTCCAG- 599
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QY 1015 GCTGCGTGGCTGTATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGGGCCCT 1074
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QY 1075 ATCATGTGAAGTTCGGCTCACTCTCCA 1101
Db 1310 ACCATGAGAAGTTCGGTCCCTGAACA 1336

RESULT 13
AF475086
LOCUS
DEFINITION Mus musculus mucolipin-3 (Mcoln3) mRNA, complete cds.
ACCESSION AF475086
VERSION AF475086.1 GI:19072755
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1712)
AUTHORS Falardeau,J.L., Kennedy,J.C., Acierno,J.S. and Slaugenhaupt,S.A.
TITLE Cloning of the mouse Mcoln3 gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1712)
AUTHORS Falardeau,J.L., Kennedy,J.C., Acierno,J.S. and Slaugenhaupt,S.A.
TITLE Direct Submission
JOURNAL Submitted (24-JAN-2002) Molecular Neurogenetics, Harvard Institute
of Human Genetics, 77 Ave. Louis Pasteur, HIM Building Room 422,
Boston, MA 02115, USA

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454 a 412 c 402 g 444 t

BASE COUNT
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Query Match 28.9%; Score 317.8; DB 10; Length 1712;
Best Local Similarity 58.1%; Pred. No. 3.8e-49;
Matches 643; Conservative 0; Mismatches 422; Indels 42; Gaps 3;
QY 1 CATTCCGGGAAGAGAAACACCATCGCCTTCCGACACCTCTTCTGCTGGGCTACTCGGACG 60
Db 268 CTTTCAAAGAGAGAAACACTATAGCCTTCAACACCTCTTCTTAAGGGCTACATGGATC 327
QY 61 GAGCGGATGACACCTTCCGAGCCCTACACGGGGAGCAGCTGTACACGGCCATCTTCCATG 120
Db 328 GAATGGACGACACCTATGCAGTGTACACTCAGAGTGAAGTGTATGACCATCATCTTTG 387
QY 121 CTGTGGACCACTACCTGGCGTTGCCCTGACGTGTCACTGGGCGGTATGCGTATGTCCGTG 180
Db 388 CAGTGACCCAGTACTTGCAGCTTCAGAACATCTCCGTGGGCAATCACGCTTAT----- 440
QY 181 GTGGGGTGAACCTTGGACCAATGGCTCAGGGCTTGTCTCTGSCAGCGGTACTACCACC 240
Db 441 -----GAGAACAAAGGGGACTAAGCAGTCGGCGATGGCAATCTGTACGCACTTCTACAGGC 495
QY 241 GAGGCCACGTGGACCCCGGCCAACGACACATTTGACATTTGATCCGATGGTGTACTGACT 300
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QY 301 GCATCCAGGTGGATCCCCCGAGCGGCCCTTCCGCCCCCAGGACGATCTCACCCCTCT 360
Db 556 GTTTCCTTTAGAGCCAGATGAAGCTTCCCACCTTGGAACGCCCTGGAGAAAATAAATC- 614
QY 361 TGGAAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAAATTCACAAGCTGGTCAATGTCA 420
Db 615 -----AACCTGAGCCTGGACTTCCACAGACTTCTGACGGTGG 651
QY 421 CCATCCACTTCCGGCTGAAGACCAATTAACCTCCAGAGCCTCATCAATAATGAGATCCCGG 480
Db 652 AGCTCCAGTTTAACTCAAAGCCCATCAATCTGCAGACAGTTCCGACACCGAGGCTTCCGTG 711
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Db 712 ACTGTTACGACTTACGCTGACTATAACATTCGACAAACAAGGCTCAGTGAAGAATCA 771
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RESULT 14
AF475085
LOCUS AF475085 1900 bp mRNA linear PRI 03-MAR-2002
DEFINITION Homo sapiens mucolipin-3 (MCOLN3) mRNA, complete cds.
ACCESSION AF475085
VERSION AF475085.1 GI:19072753
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1900)
AUTHORS Falardeau,J.L., Kennedy,J.C., Acierno,J.S. and Slaugenhaupt,S.A.
TITLE Cloning of the MCOLN3 gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1900)
AUTHORS Falardeau,J.L., Kennedy,J.C., Acierno,J.S. and Slaugenhaupt,S.A.
TITLE Direct Submission
JOURNAL Submitted (24-JAN-2002) Molecular Neurogenetics, Harvard Institute of Human Genetics, 77 Ave. Louis Pasteur, HIM Building Room 422, Boston, MA 02115, USA

FEATURES
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BASE COUNT 562 a 380 c 377 g 581 t
ORIGIN

Query Match 27.1%; Score 298.6; DB 9; Length 1900;
Best Local Similarity 57.0%; Pred. No. 1.4e-45;
Matches 631; Conservative 0; Mismatches 434; Indels 42; Gaps 3;

QY 1 CATTCCGGGAAGAGAACACCATCGCTTCGACACCTCTCTCTGCTGGGCTACTCGGACG 60
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Db 547 GAGGAAACATCTACCTCTGAAATGATACCTTTGACATCGATCCAGAAATGAAACTGAGT 606
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LOCUS BD156806 1762 bp DNA linear PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD156806
VERSION BD156806.1 GI:27862564
KEYWORDS JP 2002191363-A/11649.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1762) Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 11649 09-JUL-2002; HELIX RESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002191363-A/11649 PD 09-JUL-2002 PF 28-JUL-2000 JP 2000280990 PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU PI SAITO, PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU, PI KEIICHI NAGAI,TETSUJI OTSUKI PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ 10, C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers FT CDS (54)..(1544). source Location/Qualifiers 1..1762 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" BASE COUNT 516 a 351 c 347 g 548 t ORIGIN

Query Match 23.7%; Score 260.8; DB 6; Length 1762; Best Local Similarity 57.6%; Pred. No. 1.5e-38; Matches 525; Conservative 0; Mismatches 357; Indels 30; Gaps 2; QY 196 GGACCAATGGCTCAGGGTTGCTCTCTGCCAGGGTACTACCACCGAGGCCACGTGGACC 255 Db 334 GTACCAAGCAATCTGCTATGGCAATCTGTCCAGCACTTCTACAAGCGAGGAAACATCTACC 393 QY 256 CGGCCAACGACACATTGACATTGATCCGATGGTGTACTGACTGCATCCAGGTGGATC 315 Db 394 CTGGAATGATACCTTTGACATCGATCCAGAATTGAACCTGAGTGTCTTTGTGGAGC 453 QY 316 CCCCCGAGGGCCCCCTCCGCCCCCCCAGCGACGATCTCACCCCTCTTGGAAAGCAGCTCCA 375 Db 454 CAGATGAACC-----TTTTCACATTGGGACACCAGCAGAAA 489 QY 376 GTTACAAGAACCTCAGCTCAAATTCACAAGCTGGTCAATGTCAACATCCACTTCCGGC 435 Db 490 ATAAACTGAACCTTAACACTGGACTTCCACAGACTCCTAAACAGTGGAGCTCAGTTTAAAC 549 QY 436 TGAAGACCATTAACCTCCAGAGCCTCATCAATAATAGATCCCGGACTGCTATACCTTCA 495 Db 550 TGAAGGCCATTAAATCTGCAGACAGTTCGTTCATCAAGAAGTCCCTGACTGTATGACTTTA 609 QY 496 GCGTCCTGATCACGTTTGACAACAAAGCACACAGTGGCGGATCCCCATCAGCCTGGAGA 555 Db 610 CTCTGACTATAACATTGACAACAAGGCCCATAGTGAAGAAATTAATAAGTTTAGATA 669 QY 556 CCCAGGCCACATCCAGGAGTGTA-----GCACCCAGTGTCTTCCAGCACGGAGACA 609 Db 670 ATGACATTTCCATCAGAGAATGTAAAGACTGGCATGTATCTGGATCAATTCAGAAGAACA 729 QY 610 ACAGCTTCGGGCTCCTGTTTGACGTGGTGGTCACTCCTCACCTGCTCCCTGCTCCTCC 669 Db 730 CTCATTACATGATGATCTTTGATGCCCTTTGTCAATCTGACTTGTCTTGGTTTCATTAATCC 789 QY 670 TCTGCGCCCGCTCACTCCCTTCGAGGCTTCCCTGTCAGAACAGAGTTTGTGGGTTTCATGT 729 Db 790 TCTGCATTAGATCTGTGATTAGAGGACTTCAGCTTCAGCAGGAGTTTGTCAATTTTTC 849 QY 730 GCGCGCAGCGGGACGGGTGATCAGCCTGTGGGAGCGGCTGGAATTTGTCAATGGCTGGT 789

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	142.4	70.8	1740	13	US-10-103-458-3
3	142.4	70.8	2052	10	US-09-965-529-50
4	142.4	70.8	2052	11	US-09-969-680A-50
5	142.4	70.8	2094	9	US-09-820-893-26
6	142.4	70.8	2095	9	US-09-828-466-1
7	142.4	70.8	2095	13	US-10-103-458-1
8	122.4	60.9	1827	11	US-09-866-050A-608
9	122.4	60.9	1827	14	US-10-152-661-608
10	121.4	60.4	463	11	US-09-918-995-27041
11	54	26.9	531	9	US-09-864-761-12313
12	52.4	26.1	1912	11	US-09-796-753-161
13	50.4	25.1	207	9	US-09-864-761-28893
14	42	20.9	668	11	US-09-764-872-676
15	41.4	20.6	1677	12	US-10-305-810-4
16	41.4	20.6	1677	12	US-10-114-153-21

C 17	41.2	20.5	1520	11	US-09-992-600A-107	Sequence 107, App
C 18	41.2	20.5	1520	11	US-09-924-340-107	Sequence 107, App
C 19	41.2	20.5	1520	12	US-09-992-095B-107	Sequence 107, App
C 20	41.2	20.5	1520	12	US-10-154-678-107	Sequence 107, App
C 21	41.2	20.5	1520	12	US-09-999-570-107	Sequence 107, App
C 22	41.2	20.5	1520	14	US-10-000-489-107	Sequence 107, App
C 23	41.2	20.5	1520	14	US-10-000-986-107	Sequence 107, App
C 24	41.2	20.5	1528	11	US-09-746-783-183	Sequence 183, App
C 25	41.2	20.5	1554	14	US-10-037-270-802	Sequence 802, App
C 26	40.6	20.2	1671	12	US-10-114-153-23	Sequence 23, Appl
C 27	40.6	20.2	2067	12	US-10-114-153-27	Sequence 27, Appl
C 28	40.6	20.2	2130	12	US-10-114-153-25	Sequence 25, Appl
C 29	40.2	20.0	594	12	US-10-140-472-10	Sequence 10, Appl
C 30	40.2	20.0	594	12	US-10-141-761-10	Sequence 10, Appl
C 31	40.2	20.0	594	12	US-10-142-885-10	Sequence 10, Appl
C 32	40.2	20.0	594	12	US-10-158-790-10	Sequence 10, Appl
C 33	40.2	20.0	594	14	US-10-123-155-10	Sequence 10, Appl
C 34	40.2	20.0	594	15	US-10-146-731-10	Sequence 10, Appl
C 35	40	19.9	1470	14	US-10-156-761-5816	Sequence 5816, Ap
C 36	40	19.9	9025608	14	US-10-156-761-1	Sequence 1, Appli
C 37	37.2	18.5	1926	12	US-10-294-804-3	Sequence 3, Appli
C 38	37.2	18.5	8705	14	US-10-291-230-14	Sequence 14, Appl
C 39	37.2	18.5	8705	14	US-10-291-249-14	Sequence 14, Appl
C 40	37.2	18.5	9600	12	US-10-278-751-1	Sequence 1, Appli
C 41	37.2	18.5	10233	12	US-10-050-898-283	Sequence 283, App
C 42	37.2	18.5	10285	12	US-10-050-902-283	Sequence 283, App
C 43	36	17.9	1506	14	US-10-156-761-5159	Sequence 5159, Ap
C 44	35.2	17.5	1882	14	US-10-037-270-427	Sequence 427, App
C 45	34.4	17.1	1224	12	US-09-953-348-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-09-828-466-3
; Sequence 3, Application US/09828466
; Patent No. US20020035056A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
; FILE REFERENCE: MNI-125CP
; CURRENT APPLICATION NUMBER: US/09/828,466
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/544,797
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1740)
US-09-828-466-3

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QY	118	CATGTTTGTGACGTTTCGCCGCCATCAGGGCCGACAGGGCCGACGAGCCCTGGTGTGGCT	177	
Db	1416	CATGTTTGTGACGTTTCGCCGCCATCAGGGCCGACAGGGCCGACGAGCCCTGGTGTGGCT	1475	
QY	178	CTTCTCCAGCTCTACCTTTACTC	201	
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; Sequence 3, Application US/10103458
; Publication No. US20020197680A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
; FILE REFERENCE: MNI-125
; CURRENT APPLICATION NUMBER: US/10/103,458
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US/09/544,797
; PRIOR FILING DATE: PEIOE FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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US-10-103-458-3

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QY      118 CATGTTTGTGACGTTCCGCCCATGCAGGCGCAGAGCCGCGCAGAGCCTGGTGTGGCT 177
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Db      1416 CATGTTTGTGACGTTCCGCCCATGCAGGCGCAGAGCCGCGCAGAGCCTGGTGTGGCT 177
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QY      178 CTTCTCCCAGCTCTACCTTTACTC 201
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RESULT 3
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; Sequence 50, Application US/09965529
; Publication No. US20020182671A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731 USA
; CURRENT APPLICATION NUMBER: US/09/965,529
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 50
; LENGTH: 2052
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 977658CB1
US-09-965-529-50

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QY      118 CATGTTTGTGACGTTCCGCCCATGCAGGCGCAGAGCCGCGCAGAGCCTGGTGTGGCT 177
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QY      178 CTTCTCCCAGCTCTACCTTTACTC 201
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Db      1583 CTTCTCCCAGCTCTACCTTTACTC 1606
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RESULT 4
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; Sequence 50, Application US/09969680A
; Publication No. US20030124649A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti; YUE, Henry
; APPLICANT: TANG, Y. Tom; BANDMAN, Olga
; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731-1 USA
; CURRENT APPLICATION NUMBER: US/09/969,680A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US00/22315
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/149,641
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/164,203
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 50
; LENGTH: 2052
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124649A1 977658CB1
US-09-969-680A-50

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QY      178 CTTCTCCCAGCTCTACCTTTACTC 201
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; Sequence 26, Application US/09820893
; Patent No. US20020076705A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 31 Human Secreted Proteins
; FILE REFERENCE: P2033P1
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					Gaps 0;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201	100.0	11365	22	AAK73827 Human immune/haema
2	201	100.0	20046	22	AAK73826 Human immune/haema
3	143.4	71.3	3371	23	AAS89322 DNA encoding novel
4	143.2	71.2	318	23	AAS89310 DNA encoding novel
5	143.2	71.2	2092	23	AAS72274 DNA encoding novel
6	142.4	70.8	1740	24	ABL40755 Human TLCC-2 prote
7	142.4	70.8	1740	24	AAI71700 Human TRP-like cal
8	142.4	70.8	1741	22	AAI59236 Human polynucleoti

9	142.4	70.8	2052	22	AAF81753 Human membrane ass
10	142.4	70.8	2092	24	ABL90358 Human polynucleoti
11	142.4	70.8	2094	21	AA339067 Human secreted pro
12	142.4	70.8	2095	24	ABL40754 Human TLCC-2 prote
13	142.4	70.8	2095	24	AAI71699 Human TRP-like cal
14	140.8	70.0	635	23	AAS89318 DNA encoding novel
15	131.4	65.4	1619	22	AAI61022 Human polynucleoti
16	122.4	60.9	1827	24	ABL35079 Murine cDNA isolat
17	54	26.9	531	22	AAK08799 Human brain expres
18	54	26.9	531	22	AAI40407 Probe #9093 used t
19	54	26.9	531	23	ABS34459 Human liver single
20	52.4	26.1	1762	22	AAH14814 Human cDNA sequenc
21	52.4	26.1	1912	22	AAS01697 Human TANGO 480 cd
22	50.4	25.1	207	22	AAK21491 Human brain expres
23	50.4	25.1	207	22	AAI53486 Probe #22172 used
24	50.4	25.1	207	23	ABS47387 Human liver single
25	46.4	23.1	499	23	AAS72273 DNA encoding novel
26	42	20.9	668	22	AAS39779 Genomic sequence #
27	42	20.9	668	22	AAK90132 Human digestive sy
28	41.4	20.6	1677	25	ABX56271 Human NOV9a CG9070
29	41.2	20.5	1468	21	AAA95496 Hela cell library
30	41.2	20.5	1520	25	ACC51113 Human JNK3-binding
31	41.2	20.5	1528	20	AA335555 Secreted protein c
32	41.2	20.5	1554	22	AAI58910 Human polynucleoti
33	41.2	20.5	1749	22	AAI60696 Human polynucleoti
34	40.6	20.2	492	22	ABA08523 Human secreted pro
35	40.6	20.2	1671	25	ABX56272 Human NOV9b CG9070
36	40.6	20.2	2067	25	ABX56274 Human NOV9d CG9070
37	40.6	20.2	2130	25	ABX56273 Human NOV9c CG9070
38	39.6	19.7	2194	23	ABL29717 Drosophila melanog
39	39.6	19.7	5035	23	ABL29716 Drosophila melanog
40	37.2	18.5	799	19	AAV55831 Nucleotide sequenc
41	37.2	18.5	1925	20	AA90924 Epstein Barr Virus
42	37.2	18.5	1926	21	AA50254 Epstein Barr virus
43	37.2	18.5	1926	22	AAF82902 EBV tethering prot
44	37.2	18.5	2580	21	AA75454 Nucleotide sequenc
45	37.2	18.5	2580	24	AAI64275 Epstein-Barr virus

ALIGNMENTS

RESULT 1	
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ID	AAK73827 standard; DNA; 11365 BP.
XX	
AC	AAK73827;
XX	
DT	07-NOV-2001 (first entry)
XX	
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28639.
XX	
KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW	cytostatic; gene therapy; vaccine; metastasis; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200157182-A2.
XX	
PD	09-AUG-2001.
XX	
PF	17-JAN-2001; 2001WO-US01354.
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PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
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PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX
PS Disclosure; SEQ ID NO 28639; 3071pp + Sequence Listing; English.
XX
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome

CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 11365 BP; 2407 A; 3320 C; 3153 G; 2485 T; 0 other;

Query Match 100.0%; Score 201; DB 22; Length 11365;
Best Local Similarity 100.0%; Pred. No. 6.3e-44;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAGCCCCCGGTTCTTGGCCCATGCCTTGGTCCCTCTGACCCCGCGCCCTCTGGCA 60
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7641 GTTCCGCTCACTCTCCATGGTGTCTGAGTGCCTGTCTCGCTCATCAATGGGACGACAT 7700

QY 121 GTTTGTGACGTTCCGCGCCATGCGAGGCGCAGAGGGCGCGAGCGCTGGTGTGGCTCTT 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY 181 CTCCCAGCTCTACCTTTACTC 201
Db ||||||||||||||||||||||||||||
7761 CTCCCAGCTCTACCTTTACTC 7781

RESULT 2
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ID AAK73826 standard; DNA; 20046 BP.
XX
AC AAK73826;
XX
DT 07-NOV-2001 (first entry)
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28638.
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
KW Homo sapiens.
XX
OS WO200157182-A2.
XX
PN 09-AUG-2001.
XX
PD 17-JAN-2001; 2001WO-US01354.
XX
PF 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
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PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
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PR 08-NOV-2000; 2000US-0246477.
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PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 28638; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic

CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 20046 BP; 4133 A; 5821 C; 5659 G; 4433 T; 0 other;
Query Match 100.0%; Score 201; DB 22; Length 20046;
Best Local Similarity 100.0%; Pred. No. 6.9e-44;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCCAGCCCCGGTTCCTGCGCCATGCTTGGCTCCCTCTGACCCCGCGCCCTCTGGCA 60
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Db 7601 CCCCAGCCCCGGTTCCTGCGCCATGCTTGGCTCCCTCTGACCCCGCGCCCTCTGGCA 7660
|||
QY 61 GTTCCGCTCACTCTCCATGGTGTCTGAGTGCCTGTTCTCGCTCATCAATGGGGACGACAT 120
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Db 7661 GTTCCGCTCACTCTCCATGGTGTCTGAGTGCCTGTTCTCGCTCATCAATGGGGACGACAT 7720
|||
QY 121 GTTTGTGACGTTCCGCCCATGCGCCATGCGAGCGGCGGAGGCGGCGGCTGTTGTGGCTCTT 180
|||
Db 7721 GTTTGTGACGTTCCGCCCATGCGCCATGCGAGCGGCGGAGGCGGCGGCTGTTGTGGCTCTT 7780
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QY 181 CTCCAGCTCTACCTTTACTC 201
|||
Db 7781 CTCCAGCTCTACCTTTACTC 7801

RESULT 3

AAS89322

ID AAS89322 standard; cDNA; 3371 BP.

XX AAS89322;

AC AAS89322;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #25126.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX P-PSDB; ABG25135.

XX New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity -

XX Claim 1; SEQ ID No 25126; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 3371 BP; 842 A; 918 C; 907 G; 704 T; 0 other;

Query Match 71.3%; Score 143.4; DB 23; Length 3371;
Best Local Similarity 96.1%; Pred. No. 1e-28;
Matches 147; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 49 GCCCCTCTGGCAGTCCGCTCACTCTCATGGTGTCTGAGTGCCTGTTCTCGCTCATCAA 108
Db |||||
585 GCGCCACACGATGTTCCGCTCACTCTCATGGTGTCTGAGTGCCTGTTCTCGCTCATCAA 644
QY 109 TGGGGACGACATGTTTGTGACGTTCCGCCCATGCAGGCGCAGCAGGGCCGCGAGCCCT 168
Db |||||
645 TGGGGACGACATGTTTGTGACGTTCCGCCCATGCAGGCGCAGCAGGGCCGCGAGCCCT 704
QY 169 GGTGTGGCTCTTCTCCAGCTCTACCTTTACTC 201
Db |||||
705 GGTGTGGCTCTTCTCCAGCTCTACCTTTACTC 737

RESULT 4

AAS89310
ID AAS89310 standard; cDNA; 318 BP.

XX AC AAS89310;

XX 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #25114.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX P-PSDB; ABG25123.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

XX Claim 1; SEQ ID No 25114; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 318 BP; 52 A; 109 C; 76 G; 81 T; 0 other;

Query Match 71.2%; Score 143.2; DB 23; Length 318;
Best Local Similarity 92.1%; Pred. No. 7.7e-29;
Matches 151; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 38 CTGACCCCGCCCTCTGSCAGTTCGCTCACTCTCCATGGTGTCTGAGTGCCTGTTTC 97
Db |||||
79 CTGACCTTCTCCACAACACTATTCGCTCACTCTCCATGGTGTCTGAGTGCCTGTTTC 138
QY 98 TCGCTCATCAATGGGACGACATGTTTGTGACGTTCCGCCCATGCAGGCGCAGCAGGGC 157
Db |||||
139 TCGCTCATCAATGGGACGACATGTTTGTGACGTTCCGCCCATGCAGGCGCAGCAGGGC 198
QY 158 CGCAGCAGCCTGGTGTGGCTCTTCTCCAGCTCTACTTTACTC 201
Db |||||
199 CGCAGCAGCCTGGTGTGGCTCTTCTCCAGCTCTACTTTACTC 242

RESULT 5

AAS72274
ID AAS72274 standard; cDNA; 2092 BP.

XX AC AAS72274;

XX 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #8078.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX P-PSDB; ABG08087.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

XX
PS Claim 1; SEQ ID No 8078; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2092 BP; 386 A; 668 C; 605 G; 433 T; 0 other;

Query Match 71.2%; Score 143.2; DB 23; Length 2092;
Best Local Similarity 92.1%; Pred. No. 1.1e-28;
Matches 151; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 38 CTGACCCCGCCGCTCTGGCAGTTCGGCTCACTCTCCATGGTGTCTGAGTGCCTGTTTC 97
Db |||||
1460 CTGACCTTCTTCCACAACTACAATTCCGCTCACTCTCCATGGTGTCTGAGTGCCTGTTTC 1519

QY 98 TCGCTCATCATGGGACGACATGTTGTGACGTTTCGCCCATGCAGGGCGAGGAGGC 157
Db |||||
1520 TCGCTCATCATGGGACGACATGTTGTGACGTTTCGCCCATGCAGGGCGAGGAGGC 1579

QY 158 CGCAGCAGCCTGTGTGGCTCTTCTCCAGCTCTACCTTTACTC 201
Db |||||
1580 CGCAGCAGCCTGTGTGGCTCTTCTCCAGCTCTACCTTTACTC 1623

RESULT 6
ABL40755
ID ABL40755 standard; cDNA; 1740 BP.
XX
AC ABL40755;
XX
DT 03-JUL-2002 (first entry)
XX
DE Human TLCC-2 protein coding sequence.
XX
KW Transient receptor potential like calcium channel; TRP; TLCC-2; human;
KW neuroprotective; analgesic; nootropic; antiparkinsonian; antidepressant;
KW cerebroprotective; anxiolytic; antinomic; anticonvulsant; gene therapy;
KW calcium signaling; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1740
FT /*tag= a
FT /product= "TLCC-2"
FT /note= "transient receptor potential-like calcium
FT channel"
XX
PN US2002035056-A1.
XX
PD 21-MAR-2002.
XX
PF 06-APR-2001; 2001US-0828466.

XX
PR 07-APR-2000; 2000US-0544797.
XX
PA (CURT/) CURTIS R A J.
PA (SILO/) SILOS-SANTIAGO I.
XX
PI Curtis RAJ, Silos-Santiago I;
XX
DR WPI; 2002-338931/37.
DR P-PSDB; ABB07816.
XX
PT New nucleic acid designated TLCC-2 encodes a transient receptor
PT potential-like calcium channel and is useful to diagnose and treat pain
PT disorders and central nervous system neurodegenerative and neurological
PT disorders -
XX
PS Claim 1; Fig 1A-B; 70pp; English.
XX
CC The invention relates to a novel transient receptor potential (TRP)-like
CC calcium channel, designated TLCC-2 and polynucleotides encoding the
CC TLCC-2. TLCC-2 can be expressed by standard recombinant methodology. The
CC TLCC-2 polypeptide, polynucleotides and modulators are useful for
CC treating central nervous system disorders such as neurodegenerative
CC disorders for example Alzheimer's disease, Parkinson's disease, multiple
CC sclerosis, amyotrophic lateral sclerosis, progressive supranuclear palsy,
CC epilepsy, Creutzfeldt-Jakob disease, AIDS-related dementia, familial
CC infantile convulsions, paroxysmal choreoathetosis, psychiatric disorders
CC such as depression, anxiety, schizophrenia, psychoses, mania or phobic
CC disorders, learning or memory disorders such as amnesia, age-related
CC memory loss, or a neurological disorder such as migraine. The molecules
CC are also useful to treat a pain disorder. The present sequence represents
CC the coding sequence of the human TLCC-2 polypeptide.
XX
SQ Sequence 1740 BP; 319 A; 578 C; 475 G; 368 T; 0 other;

Query Match 70.8%; Score 142.4; DB 24; Length 1740;
Best Local Similarity 99.3%; Pred. No. 1.7e-28;
Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 GCAGTTCCGCTCACTCTCCATGGTGTCTGAGTGCCTGTCTCGCTCATCAATGGGACGA 117
Db |||||
1356 GAAGTTCCGCTCACTCTCCATGGTGTCTGAGTGCCTGTCTCGCTCATCAATGGGACGA 1415

QY 118 CATGTTTGTGACGTTTCGCCCATGCAGGGCGAGGCGGCGAGCAGCCTGTGTGGCT 177
Db |||||
1416 CATGTTTGTGACGTTTCGCCCATGCAGGGCGAGGCGGCGAGCAGCCTGTGTGGCT 1475

QY 178 CTTCTCCAGCTCTACCTTTACTC 201
Db |||||
1476 CTTCTCCAGCTCTACCTTTACTC 1499

RESULT 7
AAI71700
ID AAI71700 standard; cDNA; 1740 BP.
XX
AC AAI71700;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human TRP-like calcium channel TLCC-2 coding sequence #2.
XX
KW Human; TLCC-2; TRP-like calcium channel; membrane excitability;
KW nociception; nootropic; neuroprotective; antiparkinsonian; cytostatic;
KW hypotensive; antidepressant; analgesic; anticonvulsant; tranquiliser;
KW Parkinson's disease; Huntington's disease; multiple sclerosis;
KW Gilles de la Tourette's syndrome; autonomic function disorder; cancer;
KW neuroleptic; gene therapy; Alzheimer's disease; CNS disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1740

DE Human membrane associated protein MEMAP-13 encoding cDNA.
XX
KW Human; membrane associated protein; MEMAP; diagnosis; cytostatic;
KW antiinflammatory; anticonvulsant; immunosuppressive; antidiarrheic;
KW antiarteriosclerotic; gene therapy; cell proliferative disorder;
KW autoimmune disorder; inflammatory disorder; neurological disorder;
KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;
KW epilepsy; diarrhoea; ss.
XX
OS Homo sapiens.
XX
PN WO200112662-A2.
XX
PD 22-FEB-2001.
XX
PF 14-AUG-2000; 2000WO-US22315.
XX
PR 17-AUG-1999; 99US-0149641.
PR 09-NOV-1999; 99US-0164203.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;
PI Baughn MR, Lu DAM, Patterson C;
XX
DR WPI; 2001-168860/17.
DR P-PSDB; AAB74707.
XX
PT Isolated polypeptide with a human membrane associated protein sequence
PT is useful for the diagnosis, prevention and treatment of cell
PT proliferative, autoimmune/inflammatory, neurological and
PT gastrointestinal disorders -
XX
PS Claim 5; Page 157-158; 173pp; English.
XX
CC AAF81741 to AAF81777 encode the human membrane associated proteins
CC (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,
CC antiinflammatory, anticonvulsant, immunosuppressive, antidiarrheic and
CC antiarteriosclerotic activities, which can be used in gene therapy.
CC MEMAPs and agonist of MEMAPs can be used to treat a disease or condition
CC associated with decreased expression of functional MEMAP and antagonists
CC of MEMAP are used to treat a disease or condition associated with
CC overexpression of functional MEMAP. These disorders include cell
CC proliferative, autoimmune/inflammatory, neurological and gastrointestinal
CC disorders. The MEMAP polynucleotides and proteins are also used for the
CC diagnosis of these disorders. Specific examples of these disorders
CC include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea.
CC MEMAP proteins can be used to screen for compounds which specifically
CC bind MEMAP including antibodies, oligonucleotides, proteins and small
CC molecules. MEMAP polynucleotides can be used to prepare transgenic
CC animals which can be studied to provide information concerning human
CC disease. Anti-MEMAP antibodies are useful in immunoassays for the
CC detection of MEMAP protein and can be used as antagonists to treat or
CC prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
CC can be delivered to target cells with genetic abnormalities with respect
CC to the expression of MEMAP to treat or prevent a disorder associated
CC with MEMAP.
XX
SQ Sequence 2052 BP; 375 A; 670 C; 582 G; 425 T; 0 other;
Query Match 70.8%; Score 142.4; DB 22; Length 2052;
Best Local Similarity 99.3%; Pred. No. 1.8e-28;
Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 58 GCAGTTCGGCTCACTCTCCATGGTGTCTGAGTGCCTGTCTCGCTCATCAATGGGGACGA 117
DB 1463 GAAGTTCGGCTCACTCTCCATGGTGTCTGAGTGCCTGTCTCGCTCATCAATGGGGACGA 1522
QY 118 CATGTTTGACGCTTCGCCGCCATGCAGGGCGCAGAGGGCGCGAGAGCCTGGTGTGCT 177
DB 1523 CATGTTTGACGCTTCGCCGCCATGCAGGGCGCAGAGGGCGCGAGAGCCTGGTGTGCT 1582
QY 178 CTTCCTCCAGCTCTACCTTTACTC 201

DB 1583 CTTCTCCAGCTCTACCTTACTC 1606
RESULT 10
ABL90358
ID ABL90358 standard; cDNA; 2092 BP.
XX
AC ABL90358;
XX
DT 24-MAY-2002 (first entry)
XX
DE Human polynucleotide SEQ ID NO 920.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200190304-A2.
XX
PD 29-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-US16450.
XX
PR 19-MAY-2000; 2000US-205515P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-122018/16.
DR P-PSDB; ABB89949.
XX
PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders -
XX
PS Claim 4; SEQ ID NO 920; 2081pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2092 BP; 399 A; 676 C; 590 G; 425 T; 2 other;
Query Match 70.8%; Score 142.4; DB 24; Length 2092;
Best Local Similarity 99.3%; Pred. No. 1.8e-28;
Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 58 GCAGTTCGGCTCACTCTCCATGGTGTCTGAGTGCCTGTCTCGCTCATCAATGGGGACGA 117
DB 1463 GAAGTTCGGCTCACTCTCCATGGTGTCTGAGTGCCTGTCTCGCTCATCAATGGGGACGA 1522

CC disorders, learning or memory disorders such as amnesia, age-related
CC memory loss, or a neurological disorder such as migraine. The molecules
CC are also useful to treat a pain disorder. The present sequence represents
CC a cDNA encoding the human TLCC-2 polypeptide.

XX
SQ Sequence 2095 BP; 388 A; 682 C; 594 G; 431 T; 0 other;

Query Match 70.8%; Score 142.4; DB 24; Length 2095;
Best Local Similarity 99.3%; Pred. No. 1.8e-28;
Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 GCAGTTCGGCTCACTCTCCATGGTGTCTGAGTGCCTGTCTCGCTCATCAATGGGACGA 117
Db 1496 GAAGTTCCGCTCACTCTCCATGGTGTCTGAGTGCCTGTCTCGCTCATCAATGGGACGA 1555

QY 118 CATGTTTGTGACGTTCCGCCCATGCGCGCAGCGCGCAGCGAGCCTGGTGTGGCT 177
Db 1556 CATGTTTGTGACGTTCCGCCCATGCGCGCAGCGCGCAGCGAGCCTGGTGTGGCT 1615

QY 178 CTTCTCCAGCTCTACCTTTACTC 201
Db 1616 CTTCTCCAGCTCTACCTTTACTC 1639

RESULT 13

AAI71699
ID AAI71699 standard; cDNA; 2095 BP.

XX
AC AAI71699;

XX
DT 29-JAN-2002 (first entry)

XX
DE Human TRP-like calcium channel TLCC-2 coding sequence #1.

XX
KW Human; TLCC-2; TRP-like calcium channel; membrane excitability;
KW nociception; nootropic; neuroprotective; antiparkinsonian; cytostatic;
KW hypotensive; antidepressant; analgesic; anticonvulsant; tranquiliser;
KW Parkinson's disease; Huntington's disease; multiple sclerosis;
KW Gilles de la Tourette's syndrome; autonomic function disorder; cancer;
KW neuroleptic; gene therapy; Alzheimer's disease; CNS disorder; ss.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT CDS 141..1883
FT /*tag= a
FT /product= "TLCC-2"

XX
PN WO200177331-A1.

XX
PD 18-OCT-2001.

XX
PF 06-APR-2001; 2001WO-US11442.

XX
PR 07-APR-2000; 2000US-0544797.

XX
PA (MILL-) MILLENIUM PHARM INC.

XX
PI Curtis RAJ, Silos-Santiago I;

XX
DR WPI; 2002-010913/01.

XX
DR P-PSDB; AAM51858.

XX
PT Novel isolated human transient receptor potential-like calcium channel
PT protein-2 useful for treating Alzheimer's disease, depression, amnesia,
PT pain disorder, and cancer -

XX
PS Claim 1; Fig 1; 148pp; English.

XX
CC The present invention relates to the protein and coding sequences of
CC human transient receptor potential (TRP)-like calcium channel protein-2
CC (TLCC-2). The sequences can be used in the treatment of TLCC-2 related
CC disorders, including central nervous system disorders such as

CC Alzheimer's, Parkinson's and Huntington's diseases, multiple sclerosis,
CC Gilles de la Tourette's syndrome, autonomic function disorders, learning
CC or memory disorders, pain disorders and disorders of cellular
CC proliferation, including cancer. The present sequence is the TLCC-2
CC coding sequence including the 3' UTR.

XX
SQ Sequence 2095 BP; 388 A; 682 C; 594 G; 431 T; 0 other;

Query Match 70.8%; Score 142.4; DB 24; Length 2095;
Best Local Similarity 99.3%; Pred. No. 1.8e-28;
Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 GCAGTTCGGCTCACTCTCCATGGTGTCTGAGTGCCTGTCTCGCTCATCAATGGGACGA 117
Db 1496 GAAGTTCCGCTCACTCTCCATGGTGTCTGAGTGCCTGTCTCGCTCATCAATGGGACGA 1555

QY 118 CATGTTTGTGACGTTCCGCCCATGCGCGCAGCGCGCAGCGAGCCTGGTGTGGCT 177
Db 1556 CATGTTTGTGACGTTCCGCCCATGCGCGCAGCGCGCAGCGAGCCTGGTGTGGCT 1615

QY 178 CTTCTCCAGCTCTACCTTTACTC 201
Db 1616 CTTCTCCAGCTCTACCTTTACTC 1639

RESULT 14

AAI71699
ID AAS89318 standard; cDNA; 635 BP.

XX
AC AAS89318;

XX
DT 13-FEB-2002 (first entry)

XX
DE DNA encoding novel human diagnostic protein #25122.

XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX
OS Homo sapiens.

XX
PN WO200175067-A2.

XX
PD 11-OCT-2001.

XX
PF 30-MAR-2001; 2001WO-US08631.

XX
PR 31-MAR-2000; 2000US-0540217.

XX
PR 23-AUG-2000; 2000US-0649167.

XX
PA (HYSE-) HYSEQ INC.

XX
PI Drmanac RT, Liu C, Tang YT;

XX
DR WPI; 2001-639362/73.

XX
DR P-PSDB; ABG25131.

XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

XX
PS Claim 1; SEQ ID No 25122; 103pp; English.

XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical

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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:28:31 ; Search time 487.838 Seconds
(without alignments)
8305.735 Million cell updates/sec

Title: US-09-851-494B-1_COPY_5500_7000

Perfect score: 1501

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*

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13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*

14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*

15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*

16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*

17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*

18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*

19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*

20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*

22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*

24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1489	99.2	20046	AAK73826	Human immune/haema
2	1463.4	97.5	11365	AAK73827	Human immune/haema
3	232.8	15.5	776	AAK5931	DNA encoding novel
4	210	14.0	33147	AAK57282	Human immune/haema
5	209	13.9	47999	AAK52898	Human tweety homol
6	208.4	13.9	711	AAK82492	Human immune/haema
7	208.4	13.9	50000	ABA98944	Human asthma-assoc
C 8	208.2	13.9	15765	ABA17911	Human nervous syst

C 9	208.2	13.9	15765	22	ABA18250	Human nervous syst
C 10	208.2	13.9	15765	22	ABA18276	Human nervous syst
C 11	208.2	13.9	15765	22	ABA19009	Human nervous syst
C 12	208.2	13.9	21444	22	AAK89645	Human digestive sy
C 13	207.8	13.8	9359	22	AAK73225	Human immune/haema
C 14	207.6	13.8	566	23	ABV44771	Human prostate exp
C 15	207.4	13.8	54877	22	AAK86026	Human immune/haema
C 16	207.4	13.8	54877	25	ABZ74225	Secreted protein g
C 17	207.4	13.8	54877	25	ABZ67791	Human secreted pro
C 18	207	13.8	14769	22	AAK04404	Human reproductive
C 19	206.8	13.8	711	22	AAK82495	Human immune/haema
C 20	206.6	13.8	122748	24	ABT10719	Human breast cance
C 21	206.2	13.7	139389	24	ABK84795	Human cDNA differe
C 22	206	13.7	21470	23	ABK42270	Genomic sequence #
C 23	205.8	13.7	19199	22	AAK70995	Human immune/haema
C 24	205.8	13.7	20188	22	AAK73082	Human immune/haema
C 25	205.8	13.7	20188	22	AAK87550	Human immune/haema
C 26	205.8	13.7	32204	22	AAK39620	Genomic sequence #
C 27	205.8	13.7	32204	22	AAK89019	Human digestive sy
C 28	205.8	13.7	32204	22	AAK91533	Human digestive sy
C 29	205.8	13.7	32204	22	AAI57790	Human colorectal c
C 30	205.8	13.7	32204	24	ABS99967	Genomic DNA #171 e
C 31	204.8	13.6	31584	22	AAK81054	Human immune/haema
C 32	204.6	13.6	1743	22	AAK03368	Human reproductive
C 33	204.6	13.6	1743	22	AAI62586	Human breast or ov
C 34	204.6	13.6	1746	22	AAK03369	Human reproductive
C 35	204.6	13.6	1746	22	AAI62587	Human breast or ov
C 36	204.6	13.6	160771	24	ABQ88179	Human osteoblast d
C 37	204.6	13.6	222930	24	ABK84349	Human cDNA differe
C 38	204.4	13.6	486	23	ABV38984	Human prostate exp
C 39	204.4	13.6	154465	24	AAD28763	Human AKAP allelic
C 40	204.4	13.6	158245	24	AAD28762	Human AKAP allelic
C 41	204.4	13.6	161425	22	AAH02340	Human AKAP10 gene
C 42	204.4	13.6	162025	22	AAH02339	Human AKAP10 gene
C 43	204.4	13.6	162025	24	AAD28758	Human AKAP allelic
C 44	204.4	13.6	162025	24	AAD28759	Human AKAP allelic
C 45	204.2	13.6	5881	22	AAK07230	Human reproductive

ALIGNMENTS

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AC	AAK73826;
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DT	07-NOV-2001 (first entry)
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XX	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28638.
XX	
KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW	cytostatic; gene therapy; vaccine; metastasis; ds.
OS	Homo sapiens.
XX	
PN	WO200157182-A2.
XX	
PD	09-AUG-2001.
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PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 28638; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome

CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX

SQ Sequence 20046 BP; 4133 A; 5821 C; 5659 G; 4433 T; 0 other;

Query Match 99.2%; Score 1489; DB 22; Length 20046;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1500; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY	1	GCCGGACTCACAGGCCCTCCCTTCTCTGCCACAGTACCTGGCGTTGGCTGACGTGTC	60
Db	4102	GCCGGACTCACAGGCCCTCCCTTCTCTGCCACAGTACCTGGCGTTGGCTGACGTGTC	4161
QY	61	CTGGGCGGTATGCGTATGTCGGTGGTGGGCTGACCTTGGACCAATGGCTCAGGGCTT	120
Db	4162	CTGGGCGGTATGCGTATGTCGGTGGTGGGCTGACCTTGGACCAATGGCTCA-GGCTT	4220
QY	121	GCTCTCTGCCAGCGGTACTACACCGAGGCCACGTCGACCCGGCCCAACACACATTTGAC	180
Db	4221	GCTCTCTGCCAGCGGTACTACACCGAGGCCACGTCGACCCGGCCCAACACACATTTGAC	4280
QY	181	ATTGATCCGATGGTGTACTCTGAGTGGGCGAGGAGGCTTCACTGTGGGAGCCTG	240
Db	4281	ATTGATCCGATGGTGTACTCTGAGTGGGCGAGGAGGCTTCACTGTGGGAGCCTG	4340
QY	241	AGCTGCTGGGATTAAATCAACAGCTGTGGTGGGCGAGGCTTCACTGTGGGAGCCTG	300
Db	4341	AGCTGCTGGGATTAAATCAACAGCTGTGGTGGGCGAGGCTTCACTGTGGGAGCCTG	4400
QY	301	AGCACTTTGGGAGGCTGAGGAGGAGGATGCTTGGGCGAGGAGTGGTGGGAGCCTG	360
Db	4401	AGCACTTTGGGAGGCTGAGGAGGAGGATGCTTGGGCGAGGAGTGGTGGGAGCCTG	4460
QY	361	GGCCACGTAGGAAGACCTTGTCTCTACGACAAACAAATAGCTGGCGTGGTGGCGTGC	420
Db	4461	GGCCACGTAGGAAGACCTTGTCTCTACGACAAACAAATAGCTGGCGTGGTGGCGTGC	4520
QY	421	CCCTGTGTCCTCCAGCTACTCAGGAGGCTGAGGCGAGGAGGATCGCTTGGTGGGAGGTT	480
Db	4521	CCCTGTGTCCTCCAGCTACTCAGGAGGCTGAGGCGAGGAGGATCGCTTGGTGGGAGGTT	4580
QY	481	GAGGCTGCAGTAAGCTATGACCAAGCTGCTGCACTCCACCTGGGTGACAGAGTGAGACC	540
Db	4581	GAGGCTGCAGTAAGCTATGACCAAGCTGCTGCACTCCACCTGGGTGACAGAGTGAGACC	4640
QY	541	CTGTCTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA	600
Db	4641	CTGTCTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA	4700
QY	601	GCCACGTAGAAAGCAGATGTTATATTTTAAATATGGCTCATTCAGTAAACATCCGCA	660
Db	4701	GCCACGTAGAAAGCAGATGTTATATTTTAAATATGGCTCATTCAGTAAACATCCGCA	4760
QY	661	GGCCCCAGAGTGCCAGGCTGTAGGATGACCCCAACCTTGGGGAAGCACAGGAAGAAG	720
Db	4761	GGCCCCAGAGTGCCAGGCTGTAGGATGACCCCAACCTTGGGGAAGCACAGGAAGAAG	4820
QY	721	GCCACTGGGACTCTGGGGAGACCAAGCTGGCTCCCGGGCCCTTGGGCTTCCCTG	780
Db	4821	GCCACTGGGACTCTGGGGAGACCAAGCTGGCTCCCGGGCCCTTGGGCTTCCCTG	4880
QY	781	ACTCCCTGTCTTAGACTGCATCCAGGTGGATCCCGGGCCCTTCCCGGGCCCTTCCCTG	840
Db	4881	ACTCCCTGTCTTAGACTGCATCCAGGTGGATCCCGGGCCCTTCCCGGGCCCTTCCCTG	4940

QY	841	GGGACGATCTCACCCCTCTTGGAAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAAATTC	900
Db	4941	GGGACGATCTCACCCCTCTTGGAAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAAATTC	5000
QY	901	ACAACTACTGCTGCTCTCACTCGAGGGGGGCCAGGTTGGGGAGGAGCAGTACACTAGGCAC	960
Db	5001	ACAACTACTGCTGCTCTCACTCGAGGGGGGCCAGGTTGGGGAGGAGCAGTACACTAGGCAC	5060
QY	961	TCTACCCCGCAGCAACTACTTCCCTAAGTGGGAGCAGGGCCCCCCCCCGCGCTGGTGC	1020
Db	5061	TCTACCCCGCAGCAACTACTTCCCTAAGTGGGAGCAGGGCCCCCCCCCGCGCTGGTGC	5120
QY	1021	CTGCTGGGTGAGCACTTCCCTGCTCCAGTGCAGAGTCAAGTGGGAGGAGCGTGGC	1080
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QY	1081	ACTTGGGGCCGGAAGGAGCCGAGACGCCCTGACCCCTCAACCCGAGCTCCTGCTAGG	1140
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QY	1141	CTGGTCAATGTCAACCATCCACTTCCGGCTGACACCATTAACCTCCAGAGCTCATCAAT	1200
Db	5241	CTGGTCAATGTCAACCATCCACTTCCGGCTGACACCATTAACCTCCAGAGCTCATCAAT	5300
QY	1201	AATGATCCCGGACTGCTATACCTTCAAGCTTCTGAGGCCCCCGGGAAACCCACAG	1260
Db	5301	AATGATCCCGGACTGCTATACCTTCAAGCTTCTGAGGCCCCCGGGAAACCCACAG	5360
QY	1261	GGCTCCTGAGTTCAGGGGAGGAGCCTGCTCAGGAGTGTCTTGGGAGCACTGGCCAAAG	1320
Db	5361	GGCTCCTGAGTTCAGGGGAGGAGCCTGCTCAGGAGTGTCTTGGGAGCACTGGCCAAAG	5420
QY	1321	GCAAGCTGCGGGTGTATGAGGAGGAGGAGCCCGGGTCTGTCTGAGGAGTGTCTGATGTGA	1380
Db	5421	GCAAGCTGCGGGTGTATGAGGAGGAGGAGCCCGGGTCTGTCTGAGGAGTGTCTGATGTGA	5480
QY	1381	CCTTGGGGCTTGGGCTGCCAAGGTTTACTCTGCCCGCAACTGGCCCCACAGATCACGT	1440
Db	5481	CCTTGGGGCTTGGGCTGCCAAGGTTTACTCTGCCCGCAACTGGCCCCACAGATCACGT	5540
QY	1441	TTGACAAACAAAGCACACAGTGGGCGGATCCCCATCAGCCTGGAGACCCAGGCCACATCC	1500
Db	5541	TTGACAAACAAAGCACACAGTGGGCGGATCCCCATCAGCCTGGAGACCCAGGCCACATCC	5600
QY	1501	A 1501	
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RESULT 2
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ID AAK73827 standard; DNA; 11365 BP.
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AC AAK73827;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28639.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX
OS cytosolic; gene therapy; vaccine; metastasis; ds.
XX
PN Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
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PF 17-JAN-2001; 2001WO-US01354.
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PR 31-JAN-2000; 2000US-0179065.
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PR 02-MAR-2000; 2000US-0186350.
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PR 05-DEC-2000; 2000US-0251988.
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PR 06-DEC-2000; 2000US-0251479.
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PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
DR
XX
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure; SEQ ID NO 28639; 3071pp + Sequence Listing; English.
XX

PD 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
PF 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
PR (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
DR P-PSDB; ABG01744.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 1735; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 776 BP; 141 A; 243 C; 248 G; 144 T; 0 other;

Query Match 15.5%; Score 232.8; DB 23; Length 776;
Best Local Similarity 98.8%; Pred. No. 1.5e-46;
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589 GACCCCTTGACCAATGGCTCAGGGCTTGCTCTCTGCCAGCGGTACTACCCAGGCCAC 648
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QY 213 AGGACGAGGCTTCACTGTTGGGAGCCCTGAGCTGCTGGGATTAATCAACAGCTGGCT 272
Db |||||
709 AGGACGAGGCTTCACTGTTGGGAGCCCTGAGCTGCTGGGATTAATCAACAGCTGGCT 768
QY 273 GGGCAGCG 280
Db |||||
769 GGGCAGCG 776

RESULT 4
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DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22094.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
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XX
PF 17-JAN-2001; 2001WO-US01354.
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[illegible]

RESULT 5
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XX AAD52898;
XX
XX 14-MAY-2003 (first entry)
XX
XX Human tweety homologue 2 (TTYH2) gene.
XX
XX Human; tweety homologue 2; TTYH2; therapy; cancer; tumour; cytostatic;
XX diagnostic marker; gene; ds.
XX
XX Homo sapiens.
XX
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XX CDS
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XX 1936..2074
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XX /tag= d
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FT /tag= ab
FT /number= 14
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XX WO200292629-A1.
XX
XX 21-NOV-2002.
XX
XX 14-MAY-2002; 2002WO-AU00591.
XX
XX 14-MAY-2001; 2001AU-0004971.
XX (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
XX Clements JA;
XX
XX WPI; 2003-129264/12.
XX P-PSDB; AAE34613.
XX
XX New human tweety homolog 2 polypeptides and polynucleotides, useful for
XX producing an antigen-binding molecule that is immuno-interactive with
XX the polypeptide or as diagnostic markers for cancers -
XX
XX Claim 10; Page 128-156; 176pp; English.
XX
XX The invention relates to human tweety homologue 2 (TTYH2) polypeptide and
XX polynucleotide sequence. TTYH2 is useful for producing an antigen-binding
XX molecule that is immuno-interactive with the polypeptide. The agent is
XX useful for manufacturing a medicament for restoring a normal level and/or
XX functional activity of TTYH2 expression in a patient, and for treating or
XX preventing cancer or tumour. TTYH2 sequences may also be used to provide
XX both drug targets and regulators to promote or inhibit one or more
XX activities, and to provide diagnostic markers for cancers. The present
XX sequence is human TTYH2 gene.
XX
XX Sequence 47999 BP; 11178 A; 12727 C; 12874 G; 11209 T; 11 other;
XX
XX Query Match 13.9%; Score 209; DB 25; Length 47999;
XX Best Local Similarity 79.3%; Pred. No. 3.9e-40;
XX Matches 264; Conservative 0; Mismatches 60; Indels 9; Gaps 1;
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QY 251 ATTAAATCAACAGCTGTGGCTGGGCACGGTGGCTCAGCCCTATAATACCAGCACTTTGG 310
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QY 311 GAGGCTGAGGAGGAAGGATTGCTTGAGGCCAGAGTTTGAGACCAGCCCTGGGCCACGTAG 370
Db 18437 GAGGCCAGGTGGGAGAAATTGCTTGAGGCCAGGAGTTCAAGACCAGCCCTGGGCAACATAG 18496
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RESULT 6
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DT 07-NOV-2001 (first entry)
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DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37304.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
PD
XX 09-AUG-2001.
PF
XX 17-JAN-2001; 2001WO-US01354.
PR
31-JAN-2000; 2000US-0179065.
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PR 07-JUL-2000; 2000US-0215647.
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PR 26-JUL-2000; 2000US-0220963.
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PR 14-AUG-2000; 2000US-0224518.
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XX DE Human nervous system related polynucleotide SEQ ID NO 10242.
XX KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX OS Homo sapiens.
PN WO200159063-A2.
XX PD 16-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01334.
XX PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
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PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
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PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
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XX
PA (HUMA-) HUMAN GENOME SCI INC.
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XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-541565/60.
XX
PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
PT cancers and metastases -
XX
PS Disclosure; SEQ ID NO 10581; 1701pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 15765 BP; 4553 A; 3137 C; 3376 G; 4699 T; 0 other;

Query Match

13.9%; Score 208.2; DB 22; Length 15765;

Best Local Similarity 79.5%; Pred. No. 4e-40;

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ID ABAl8276 standard; DNA; 15765 BP.
XX
AC ABAl8276;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polynucleotide SEQ ID NO 10607.
XX
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
PN WO200159063-A2.
XX
PD 16-AUG-2001.
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PF 17-JAN-2001; 2001WO-US01334.
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Rosen CA, Barash SC, Ruben SM;

WPI; 2001-541565/60.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -

Disclosure; SEQ ID NO 11340; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple-sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at <ftp.wipo.int/pub/published> pct sequences.

Sequence 15765 BP; 4553 A; 3137 C; 3376 G; 4699 T; 0 other;

Query Match 13.9%; Score 208.2; DB 22; Length 15765;
Best Local Similarity 79.5%; Pred. No. 4e-40;
Matches 260; Conservative 0; Mismatches 63; Indels 4; Gaps 1;

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Dδ 4184 T G A A A G T T T A T G T A A T G G C C C G G G C A C G G T G G C T C A C A C C T A T A A T C C C A G C A C T T G G G 4125

Qy 312 AGCTGAGGAGGAAGGATTGCTTGAGGCCAGAAGTTTGAGACCAGCCTGGGCCACGTAGG 371

Db 4124 AGGCTGAGGTGGGCGGATCACCTGAGGTGAGGAGTTTGAGACCAGCCTGGCCAAAGATGGC 4065

Qy 372 AAGACCTTGCTCTACGACAA---ACAAATTAGCTGGGCGTGGTGGCGTGCCCTGTG 427

Db 4064 AAAACCCCTGCTCTACTAAAAAGTGCAAAAATTACCGGATATGGTGGTGCAACCTGTA 4005

Qy 428 GTCCAGCTACTCAGGAGGCTGAGGCAGGAGGATCGCTTGAGTCCGGGAGGCTTGAGCTG 487

Dd 4004 ATCCAGCTACTCAGGAGGCTGAGGCAGGAGGATCGCTTGAACTCCAGGAGTGGAGTTG 3945

[illegible]

Qy 548 AAAAAAAAAAAAAAAAAAAAAA 574
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Dd 3884 AAAAAAAAAAAAAAAAAAAAAA 3858
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AC	AAK89645;
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DT	05-NOV-2001 (first entry)
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DE	Human digestive system antigen genomic sequence SEQ ID NO: 3221.
XX	
KW	Human; digestive system antigen; Gene therapy; cancer; appendicitis;
KW	ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW	digestive system disorder; Meckel's diverticulum; ds.

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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
DR
XX
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure; SEQ ID NO 28037; 3071pp + Sequence Listing; English.
XX

CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX

SQ Sequence 9359 BP; 1726 A; 2741 C; 3065 G; 1827 T; 0 other;

Query Match 13.8%; Score 207.8; DB 22; Length 9359;
Best Local Similarity 77.1%; Pred. No. 4.2e-40;
Matches 266; Conservative 0; Mismatches 77; Indels 2; Gaps 1;

PR 07-JUL-2000; 2000US-0216880.
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PR 11-JUL-2000; 2000US-0217496.
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PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
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PR 05-JAN-2001; 2001US-02559678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure; SEQ ID NO 40838; 3071pp + Sequence Listing; English.
XX

CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)

CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (i) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.

XX

SQ Sequence 54877 BP; 15008 A; 10329 C; 11472 G; 18068 T; 0 other;

Query Match 13.8%; Score 207.4; DB 22; Length 54877;
Best Local Similarity 78.2%; Pred. No. 9.9e-40;
Matches 262; Conservative 0; Mismatches 71; Indels 2; Gaps 1;

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QY	314	GCTCAGGAGGAGGATTGCTTGAGGCCAGAGTTTGAGACCAGCCTGGGCCACGTAGGAA	373
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QY	374	GACCTTGCTCTACGCACAAACAAATTAGTGGGCGTGGTGGCGTCCCTGTGGTCCCA	433
Db	32143	AACCCCGTCTCTACTAAAAACACAATTAGCCAGGCGTGGTGGCGTGGCCTGTATCCCA	32084
QY	434	GCTACTCAGGAGGCTGAGGCAGGAGGATCGCTTGAGTCCGGGAGTTGAGGCTGCAGTAA	493
Db	32083	GCTACTCGGAGAGCTGAGGCAGGAGATCGCTTGAACCCGGGAGTGGAGTTGCAGTGA	32024
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QY	554	AAAAAAAAAAAAAAAAAACAAGTATGCTTAGTGTG	588
Db	31963	AAAAAAAAAAAAAAAAATCAAGGGGGCCAGGTGTG	31929

Search completed: October 27, 2003, 12:34:11
Job time : 493.838 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:10:42 ; Search time 6013.64 Seconds
(without alignments)
10211.014 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rod:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	1501	100.0	13270	9	AF287270	AF287270 Homo sapi
2	1501	100.0	173126	9	AC008878	AC008878 Homo sapi
C 3	1463.4	97.5	155645	2	AC021153	AC021153 Homo sapi
4	490	32.6	579	9	AF305572S5	AF305576 Homo sapi
5	442.6	29.5	2272	9	HSA293659	AJ293659 Homo sapi
6	332	22.1	332	9	AF305572S4	AF305575 Homo sapi
7	227	15.1	790	9	AF305572S3	AF305574 Homo sapi
C 8	224.4	15.0	164293	9	AC020978	AC020978 Homo sapi
C 9	223.6	14.9	89666	2	AC022403	AC022403 Homo sapi
10	223	14.9	155521	9	AC069335	AC069335 Homo sapi
11	223	14.9	193267	2	AC093695	AC093695 Homo sapi
C 12	221.8	14.8	166138	9	AC084756	AC084756 Homo sapi
C 13	220	14.7	162617	9	AC007501	AC007501 Homo sapi
C 14	220	14.7	169202	9	AC007490	AC007490 Homo sapi
15	219.2	14.6	59634	2	AC133460	AC133460 Homo sapi
16	218.6	14.6	89653	9	AC080096	AC080096 Homo sapi
C 17	218.6	14.6	108316	6	AX647597	AX647597 Sequence
18	218.6	14.6	170423	9	AC018663	AC018663 Human Chr
C 19	218	14.5	151964	9	AL663038	AL663038 Human DNA
C 20	218	14.5	166336	9	AL445467	AL445467 Human DNA
21	217.6	14.5	83969	9	AC005210	AC005210 citb_179
22	217.6	14.5	137718	9	AL137066	AL137066 Human DNA
C 23	216.6	14.4	194062	9	AC138071	AC138071 Homo sapi
C 24	215.8	14.4	184536	2	AC068682	AC068682 Homo sapi
25	215.8	14.4	218074	9	AC023283	AC023283 Homo sapi
C 26	215.4	14.4	95620	9	AC106753	AC106753 Homo sapi
27	214.4	14.3	188488	9	AC006057	AC006057 Homo sapi
C 28	214	14.3	153792	9	AC012073	AC012073 Homo sapi
C 29	214	14.3	162820	9	AL138765	AL138765 Human DNA
C 30	213.8	14.2	233877	9	AC093798	AC093798 Homo sapi
31	213.6	14.2	181907	2	AC108731	AC108731 Homo sapi
32	213.4	14.2	129435	9	AL391314	AL391314 Human DNA
C 33	213.2	14.2	56912	9	AL160176	AL160176 Human DNA
34	213	14.2	153223	2	AC074339	AC074339 Homo sapi
35	213	14.2	169822	2	AC144998	AC144998 Pan trogl
C 36	213	14.2	240000	2	AC008130	AC008130 Homo sapi
37	212.8	14.2	142003	9	AC098800	AC098800 Homo sapi
38	212.6	14.2	43987	9	AC005391	AC005391 Homo sapi
39	212.6	14.2	141442	9	AC108471	AC108471 Homo sapi
C 40	212.4	14.2	160420	9	AC022023	AC022023 Homo sapi
41	212.4	14.2	171309	9	AC012146	AC012146 Homo sapi
C 42	212.4	14.2	212622	9	AC025259	AC025259 Homo sapi
C 43	212.2	14.1	121739	9	AC006084	AC006084 Homo sapi
C 44	212	14.1	46774	9	AL354914	AL354914 Human DNA
45	212	14.1	86684	9	AC010605	AC010605 Homo sapi

ALIGNMENTS

RESULT 1
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LOCUS AF287270 13270 bp DNA linear PRI 30-OCT-2000
DEFINITION Homo sapiens mucopolipin (MCOLN1) gene, complete cds.
ACCESSION AF287270
VERSION AF287270.1 GI:9844925
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 13270)
AUTHORS Sun,M., Goldin,E., Stahl,S., Falardeau,J.L., Kennedy,J.C.,
Acierno,J.S. Jr., Bove,C., Kaneski,C.R., Nagle,J., Bromley,M.C.,
Colman,M., Schiffmann,R. and Slangenhuys,S.A.

TITLE Mucolipidosis type IV is caused by mutations in a gene encoding a novel transient receptor potential channel
JOURNAL Hum. Mol. Genet. 9 (17), 2471-2478 (2000)
MEDLINE 20485419
PUBMED 11030752
REFERENCE 2 (bases 1 to 13270)
AUTHORS Slaughterhaus, S.A.
TITLE Direct Submission
JOURNAL Submitted (13-JUL-2000) Molecular Neurogenetics, Harvard Institute of Human Genetics, 77 Ave. Louis Pasteur, HIM Building Room 422, Boston, MA 02115, USA

FEATURES
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/join(1526..1556,3736..3941,5214..5381,5536..5701,6295..6403,6639..6735,6933..7032,7372..7478,7596..7745,7876..7977,8365..8487,9061..9276,12298..12428,12534..12753)
/gene="MCOLN1"
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BASE COUNT 2843 a 3776 c 3737 g 2914 t
ORIGIN

Query Match 100.0%; Score 1501; DB 9; Length 13270;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCGGACTCACAGGCCCTCCCTTCTCTGCCACAGTACCTGGCGTTGCCGTGACGTGCA 60
DB 5500 GCCGGACTCACAGGCCCTCCCTTCTCTGCCACAGTACCTGGCGTTGCCGTGACGTGCA 5559
QY 61 CTGGGCGGTATGCGTATGTCGGTGGTGGGCGTGAACCTTGACCAATGGCTCAGGGCTT 120
DB 5560 CTGGGCGGTATGCGTATGTCGGTGGTGGGCGTGAACCTTGACCAATGGCTCAGGGCTT 5619
QY 121 GCTCTCTGCCAGCGGTACTACCAACCGAGCCACGTGGACCCCGCCACGACACATTGAC 180
DB 5620 GCTCTCTGCCAGCGGTACTACCAACCGAGCCACGTGGACCCCGCCACGACACATTGAC 5679
QY 181 ATTGATCCGATGGTGGTACTGCTGAGTGGGACGAGCGCTTCACTGTTGGAGCCTG 240
DB 5680 ATTGATCCGATGGTGGTACTGCTGAGTGGGACGAGCGCTTCACTGTTGGAGCCTG 5739
QY 241 AGCTGCTGGGATTAAATCAACAGCTGTGGTGGGACGCTGAGCTTCACTGTTGGAGCCTG 300
DB 5740 AGCTGCTGGGATTAAATCAACAGCTGTGGTGGGACGCTGAGCTTCACTGTTGGAGCCTG 5799

QY 301 AGCATTCTGGAGGCTGAGGAGGAGGATTCTTGGAGCCAGAAAGTTTGGAGCCAGCCTG 360
DB 5800 AGCATTCTGGAGGCTGAGGAGGAGGATTCTTGGAGCCAGAAAGTTTGGAGCCAGCCTG 5859
QY 361 GGCCACGTAGGAAGACCTTGTCTCTACGCACAAACAAATTAGCTGGGCGCTGGTGGCTGC 420
DB 5860 GGCCACGTAGGAAGACCTTGTCTCTACGCACAAACAAATTAGCTGGGCGCTGGTGGCTGC 5919
QY 421 CCCTGTGCTCCAGCTACTCAGGAGGCTGAGGAGGAGGATCGCTTGGTCCGGAGGCTT 480
DB 5920 CCCTGTGCTCCAGCTACTCAGGAGGCTGAGGAGGAGGATCGCTTGGTCCGGAGGCTT 5979
QY 481 GAGGCTGAGTAAGCTATGACACCGCTGCTGCTACTCCACCTGGGTGACAGAGTGAGACC 540
DB 5980 GAGGCTGAGTAAGCTATGACACCGCTGCTGCTACTCCACCTGGGTGACAGAGTGAGACC 6039
QY 541 CTGTCTCAAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
DB 6040 CTGTCTCAAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6099
QY 601 GCCACGTAGAAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
DB 6100 GCCACGTAGAAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6159
QY 661 GGCCACGAGAGTCCAGGCTGTGAGGAATGACCCACCTGGGGAAGCAGAGGGAAGAAG 720
DB 6160 GGCCACGAGAGTCCAGGCTGTGAGGAATGACCCACCTGGGGAAGCAGAGGGAAGAAG 6219
QY 721 GCCACTGGGAGCTCTGGGAGAGCAGGCTGGCCTCCCGGCCCCCTGAGGCGCTTCCCTG 780
DB 6220 GCCACTGGGAGCTCTGGGAGAGCAGGCTGGCCTCCCGGCCCCCTGAGGCGCTTCCCTG 6279
QY 781 ACTCCCTGCTCTAGACTGCATCCAGGTGGATCCCGGAGGCGGCCCCCTCCGCCCCCA 840
DB 6280 ACTCCCTGCTCTAGACTGCATCCAGGTGGATCCCGGAGGCGGCCCCCTCCGCCCCCA 6339
QY 841 GCGACGATCTCACCCCTCTTGGAAAGCAGCTCCAGTTACAAAGAACCTCACGCTCAAAATTC 900
DB 6340 GCGACGATCTCACCCCTCTTGGAAAGCAGCTCCAGTTACAAAGAACCTCACGCTCAAAATTC 6399
QY 901 ACAAGTACTGCTGCTCACTCGAGGGGGGCCCCAGGGTGGGAGGAGGAGGAGGAGGAGGAG 960
DB 6400 ACAAGTACTGCTGCTCACTCGAGGGGGGCCCCAGGGTGGGAGGAGGAGGAGGAGGAGG 6459
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DB 6460 TCTCACCCACCAACTACTTCCCTAAGGTGGGAGCAGGSCCCCCCCCCCGGCGCTGGTGC 6519
QY 1021 CTGCTGGGTGAGCACTTCCCTGCGAGCTGCAGAGTGCAGACGCTGGCAGGGGAGCCTGGC 1080
DB 6520 CTGCTGGGTGAGCACTTCCCTGCGAGCTGCAGAGTGCAGACGCTGGCAGGGGAGCCTGGC 6579
QY 1081 ACTTGGGGCCGGAAGGAGCCCGAAGACGCCCCCTGACCCCTACCCGAGCCTCCTGCTAGG 1140
DB 6580 ACTTGGGGCCGGAAGGAGCCCGAAGACGCCCCCTGACCCCTACCCGAGCCTCCTGCTAGG 6639
QY 1141 CTGCTCAATGTCAACCATCCATTCCGGCTGAAGACCAATTAACCTCCAGAGCCTCATCAAT 1200
DB 6640 CTGCTCAATGTCAACCATCCATTCCGGCTGAAGACCAATTAACCTCCAGAGCCTCATCAAT 6699
QY 1201 AATGAGATCCCGGAGTGTATACCTTCAGCGTCCCTGAGGCCCCCCCCCGGGAACCCACAG 1260
DB 6700 AATGAGATCCCGGAGTGTATACCTTCAGCGTCCCTGAGGCCCCCCCCCGGGAACCCACAG 6759
QY 1261 GGCTCTGAGTTCAGGGCAGGAGCCTGGTCAAGGAGTGTCTTGGAGCACTGGCCCAAGG 1320
DB 6760 GGCTCTGAGTTCAGGGCAGGAGCCTGGTCAAGGAGTGTCTTGGAGCACTGGCCCAAGG 6819
QY 1321 GCAAGCGTGGGGTGTATGAGGGAGGAGCCCCGGGGTCTCTCAGGCCACCTGTGATGTGA 1380
DB 6820 GCAAGCGTGGGGTGTATGAGGGAGGAGCCCCGGGGTCTCTCAGGCCACCTGTGATGTGA 6879
QY 1381 CCTTGGGGCTTGGGGCTGCCAAGGTTTACTCTGCCCCCAACTGGCCCCCACAGATCAGT 1440


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QY 1201 AATGAGATCCGGACTGCTATACCTTCAGCGTCTCTGAGGCCCCCGGGAACCCACAG 1260
Db 141849 AATGAGATCCGGACTGCTATACCTTCAGCGTCTCTGAGGCCCCCGGGAACCCACAG 141908
QY 1261 GGCTCCTGAGTCCAGGGCAGGACCTGGTCAAGGAGTCTCTGGGAGCACTGGCCCAAG 1320
Db 141909 GGCTCCTGAGTCCAGGGCAGGACCTGGTCAAGGAGTCTCTGGGAGCACTGGCCCAAG 141968
QY 1321 GCAAGCGTGGGGTGTATGAGGGAGGAGCCCGGGTCTGTCAAGCCACCTGTCTATGTGA 1380
Db 141969 GCAAGCGTGGGGTGTATGAGGGAGGAGCCCGGGTCTGTCAAGCCACCTGTCTATGTGA 142028
QY 1381 CCTTGGGGTGGGGTGTCCAAAGTTTACTCTGCCCCCACTGGCCCAAGATCACGT 1440
Db 142029 CCTTGGGGTGGGGTGTCCAAAGTTTACTCTGCCCCCACTGGCCCAAGATCACGT 142088
QY 1441 TTGACAAACAAAGCACACAGTGGGGGATCCCATCAGCTGGAGACCCAGGCCACATCC 1500
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QY 1501 A 1501
Db 142149 A 142149
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RESULT 3

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AC021153/c LOCUS
DEFINITION Homo sapiens chromosome 19 clone RP11-492L14, WORKING DRAFT
SEQUENCE, 20 unordered pieces.
AC021153
VERSION AC021153.6 GI:8570240
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 155645)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 155645)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Jun 17, 2000 this sequence version replaced gi:7344405.
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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H NH0492L14
----- Summary Statistics -----
Sequencing vector: M13; 82%
Sequencing vector: plasmid; 18%
Chemistry: Dye-primer ET; 77% of reads
Chemistry: Dye-terminator Big Dye; 23% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 141755 bases at least Q40
Consensus quality: 145922 bases at least Q30
Consensus quality: 148291 bases at least Q20
Insert size: 167000; agarose-fp
Insert size: 153745; sum-of-contigs
Quality coverage: 3.76 in Q20 bases; agarose-fp
Quality coverage: 4.16 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 1 1052: contig of 1052 bp in length
* 1053 1152: gap of unknown length
* 1153 2714: contig of 1562 bp in length
* 2715 2814: gap of unknown length
* 2815 4101: contig of 1287 bp in length
* 4102 4201: gap of unknown length
* 4202 7146: contig of 2945 bp in length
* 7147 7246: gap of unknown length
* 7247 9807: contig of 2561 bp in length
* 9808 9907: gap of unknown length
* 9908 12944: contig of 3037 bp in length
* 12945 13044: gap of unknown length
* 13045 16486: contig of 3442 bp in length
* 16487 16586: gap of unknown length
* 16587 20919: contig of 4333 bp in length
* 20920 21019: gap of unknown length
* 21020 26033: contig of 5014 bp in length
* 26034 26133: gap of unknown length
* 26134 30552: contig of 4419 bp in length
* 30553 30652: gap of unknown length
* 30653 35333: contig of 4681 bp in length
* 35334 35433: gap of unknown length
* 35434 39655: contig of 4222 bp in length
* 39656 39755: gap of unknown length
* 39756 44735: contig of 4980 bp in length
* 44736 44835: gap of unknown length
* 44836 55751: contig of 10916 bp in length
* 55752 55851: gap of unknown length
* 55852 67916: contig of 12065 bp in length
* 67917 68016: gap of unknown length
* 68017 77332: contig of 9316 bp in length
* 77333 77432: gap of unknown length
* 77433 94471: contig of 17039 bp in length
* 94472 94571: gap of unknown length
* 94572 113604: contig of 19033 bp in length
* 113605 113704: gap of unknown length
* 113705 134801: contig of 21097 bp in length
* 134802 134901: gap of unknown length
* 134902 155645: contig of 20744 bp in length.
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FEATURES

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1153. .2714
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2815. .4101
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4202. .7146
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7247. .9807
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9908. .12944
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13045. .16486
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16587. .20919
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21020. .26033
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26134. .30552
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30653. .35333
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35434. .39655
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Db 1011 CATCCACTTCGGCTGAGACCATTAACCTCCAGAGCCTCATCAATATGAGATCCCGGA 1070

QY 1215 CTGCTATACCTTCAGGCTCCTGGTGAGGCCGCCCGGGAACCCACA 1259

Db 1071 CTGCTATACCTTCAGGCTCCTGTATCACGTTTGACAAACAAGCACA 1115

RESULT 6

AF305572S4

LOCUS AF305572S4 332 bp DNA linear PRI 26-DEC-2000

DEFINITION Homo sapiens mucolipin 1 (MCOLN1) gene, exon 5.

ACCESSION AF305575

VERSION AF305575.1 GI:11991201

KEYWORDS

SEGMENT 4 of 8

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 332)

AUTHORS Bargal,R., Avidan,N., Ben-Asher,E., Olender,Z., Zeigler,M., Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.

TITLE Identification of the gene causing mucolipidosis type IV

JOURNAL Nat. Genet. 26 (1), 118-123 (2000)

MEDLINE 20428196

PUBMED 10973263

REFERENCE 2 (bases 1 to 332)

AUTHORS Bargal,R., Avidan,N., Ben-Asher,E., Olender,A., Zeigler,M., Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.

TITLE Direct Submission

JOURNAL Submitted (13-SEP-2000) Molecular Genetics, The Weizmann Institute of Science, P. O. Box 26, Rehovot 76100, Israel

FEATURES

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/mol_type="genomic DNA"

/db_xref="taxon:9606"

155. .263

/gene="MCOLN1"

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.4e-74;

Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATTCAAGTAAACATCCGAGGCCAGAGAGTGCCAGGCTGTAGGAATGACCCCAACCCCTG 60

QY 702 GGAAGCACAGGGAAGAGGCCACTGGGGACTCTGGGGAGACCAAGCTGGCCCTCCCGGC 761

Db 61 GGAAGCACAGGGAAGAGGCCACTGGGGACTCTGGGGAGACCAAGCTGGCCCTCCCGGC 120

QY 762 CCCCTGAGGCCCTTCCCTGACTCCCTGTCCCTTAGACTGCATCCAGTGGATCCCCCGAG 821

Db 121 CCCCTGAGGCCCTTCCCTGACTCCCTGTCCCTTAGACTGCATCCAGTGGATCCCCCGAG 180

QY 822 CGGCCCCCTCCGCCCCAGCGAGATCTCACCCCTCTTGGAAAGAGAGCTCCAGTTACAAG 881

Db 181 CGGCCCCCTCCGCCCCAGCGAGATCTCACCCCTCTTGGAAAGAGAGCTCCAGTTACAAG 240

QY 882 AACCTCAGCTCAATTCACAAAGTACTGCTGCTCACTCGAGGGGGCCAGGGTGGG 941

Db 241 AACCTCAGCTCAATTCACAAAGTACTGCTGCTCACTCGAGGGGGCCAGGGTGGG 300

QY 942 GAGGCAGCACACTAGGCACCTCTCACCCAGCA 973

Db 301 GAGGAGCACACTAGGCACTCTCACCCAGCA 332

RESULT 7

AF305572S3

LOCUS AF305572S3 790 bp DNA linear PRI 26-DEC-2000

DEFINITION Homo sapiens mucolipin 1 (MCOLN1) gene, exons 3 and 4.

ACCESSION AF305574

VERSION AF305574.1 GI:11991200

KEYWORDS

SEGMENT 3 of 8

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 790)

AUTHORS Bargal,R., Avidan,N., Ben-Asher,E., Olender,Z., Zeigler,M., Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.

TITLE Identification of the gene causing mucolipidosis type IV

JOURNAL Nat. Genet. 26 (1), 118-123 (2000)

MEDLINE 20428196

PUBMED 10973263

REFERENCE 2 (bases 1 to 790)

AUTHORS Bargal,R., Avidan,N., Ben-Asher,E., Olender,A., Zeigler,M., Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.

TITLE Direct Submission

JOURNAL Submitted (13-SEP-2000) Molecular Genetics, The Weizmann Institute of Science, P. O. Box 26, Rehovot 76100, Israel

FEATURES

Location/Qualifiers

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/db_xref="taxon:9606"

267. .434

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589. .757

/gene="MCOLN1"

/number=4

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ORIGIN

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Best Local Similarity 99.6%; Pred. No. 1.7e-47;

Matches 238; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 553 GCCGGACTCACAGGCCCTCCCTTCTCTGCCCCACAGTACCTGCGGTGCCTGACGTGTCA 612

QY 61 CTGGGCCGGTATCGGTATGTCCTGTTGGGGTGACCCCTTGACCAATGGCTCAGGGCTT 120

Db 613 CTGGGCCGGTATCGGTATGTCCTGTTGGGGTGACCCCTTGACCAATGGCTCA-GGCTT 671

QY 121 GCTCTCTGCCAGCGGTACTACCAAGGAGGCCACGTGGACCCCGCCCAACGACACATTTGAC 180

Db 672 GCTCTCTGCCAGCGGTACTACCAAGGAGGCCACGTGGACCCCGCCCAACGACACATTTGAC 731

QY 181 ATTGATCCGATGGTGGTTACTGTGAGTGGGAGGACGAGGCTTCACTGTTGGAGCCT 239

Db 732 ATTGATCCGATGGTGGTTACTGTGAGTGGGAGGACGAGGCTTCACTGTTGGAGCCT 790

RESULT 8

AC020978/c

LOCUS AC020978 164293 bp DNA linear PRI 13-MAR-2003

DEFINITION Homo sapiens chromosome 16 clone RP11-96D1, complete sequence.

ACCESSION AC020978

VERSION AC020978.10 GI:289333544

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Qy	494	GCTATGACCAAGCCTGTCTGCACCTCCACCCTGGGTGACAGAGTGTCTCTCAAAAAA	553
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Qy	554	AAAAAAAAAAAAAAAAAAAAA	571
Db	64055	AAACAAAAACAAAAAAA	64038

RESULT 9
AC022403/c

LOCUS AC022403 89666 bp DNA linear HTG 29-JAN-2002

DEFINITION Homo sapiens chromosome 15 clone CTD-2120M24 map 15q21, WORKING DRAFT SEQUENCE, 19 ordered pieces.

ACCESSION AC022403

VERSION AC022403.4 GI:8189326

KEYWORDS HTG; HTGS_PHASE2; HTGS_CANCELLED; HTGS_DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 89666)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., Kaur,A., Madan,A., Nesbitt,R., Shaffer,T. and Hood,L.

TITLE Sequencing of human chromosome 15 D15S146-D15S117 region

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 89666)
Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaffer,T. and Hood,L.

AUTHORS Direct Submission

TITLE Submitted (03-FEB-2000) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA

JOURNAL On Jun 2, 2000 this sequence version replaced gi:7158043.

COMMENT ----- Genome Center
Center: Multimegabase Sequencing Center
Center code: UWMSC
Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leerowen@systemsbiology.org
----- Summary Statistics

Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
Insert size: 75000; agarose-fp
Quality coverage: 3.0x in Q20 bases; sum-of-contigs

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

* NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1 6942: contig of 6942 bp in length
* 6943 7042: gap of unknown length
* 7043 14498: contig of 7456 bp in length
* 14499 14598: gap of unknown length

Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIP/DTB/CHR7>, send <mailto:seqgreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

SOURCE INFORMATION:
The RPlC1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P. Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)
VECTOR: pBACe3.6

VECTOR: PAGES: 8
NEIGHBORING SEQUENCE INFORMATION:

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-785H2; the clone sequenced to the right is RP4-592P3, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-723C11; actual end is at base position 46589 of RP4-592P3.

polymorphisms exist between AC069335 and AC006452.

FEATURES

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/mol_type="genomic DNA"
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/chromosome="7"
/map="7"
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18. 264
/note="match to EST AW814659 (NID:57907653)"
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265. 286
/rpt_family="(TTTTTG)n"
repeat_region
572. 854
/rpt_family="Alu"
misc_feature
805. 810
/note="match to EST BG721725 (NID:gl4000912)"
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878. 1170
/rpt_family="Alu"
repeat_region
1210. 1505
/rpt_family="Alu"
repeat_region
1508. 1818
/rpt_family="Alu"
repeat_region
1789. 1837
/rpt_family="A-rich"
repeat_region
1838. 1924
/rpt_family="L1"
repeat_region
1925. 2100
/rpt_family="Alu"
repeat_region
2093. 2130
/rpt_family="(T)n"
repeat_region
2101. 2417
/rpt_family="Alu"
repeat_region
2418. 2549
/rpt_family="Alu"
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2550. 2609
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repeat_region
2599. 2622
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2616. 2709
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2911. 3200
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3237. 3454
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repeat_region
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3662. 3850
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3665. 3850
misc_feature

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*	158967	159066:	gap of unknown length
*	159067	171696:	contig of 12630 bp in length
*	171697	171796:	gap of unknown length
*	171797	183547:	contig of 11751 bp in length
*	183548	183647:	gap of unknown length
*	183648	193267:	contig of 9620 bp in length.

FEATURES

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/chromosome="UNK"
/clone="RP11-795E24"
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1230. .2643
/note="assembly_name:Contig21"
2744. .4089
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4190. .5968
/note="assembly_name:Contig28"
6069. .7428
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7529. .8564
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10058. .12344
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18157. .19426
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19527. .21887
/note="assembly_name:Contig37"
21988. .24641
/note="assembly_name:Contig38"
24742. .27187
/note="assembly_name:Contig39"
27288. .28979
/note="assembly_name:Contig40"
29080. .30622
/note="assembly_name:Contig41"
30723. .33001
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33102. .34666
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34767. .37187
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40150. .42008
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47300. .50005
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50106. .53138
/note="assembly_name:Contig50"
53239. .56563
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56664. .58852
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58953. .61438
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Query Match

14.9%; Score 223; DB 2; Length 193267;

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Best Local Similarity   79.1%; Pred.No. 3.8e-46;
Matches 265; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy      243 CTGCTGGGATTAAAAATCAACAGCTGTGTGGCTGGGCACGGTCGCTCACGCCCTATAATACCAG 302
         ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      4548 CCGAGGAGCTGAGAAATGAATTGGTAAGGCCCCAGCATGGTGGCCCCACATCTGTAGTCCCAG 4607

Qy      303 CACTTTGGGACGCTGAGGAGGAAGATTGCTTGAGGCCAGAAGTTTGAGACCAGCCTGGG 362
         ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      4608 CATTTGGGAGGCTGAGGTGGGAGGATGGCTTGAGGCCAAGGAGTTTGAGACCAGCCTGGG 4667

Qy      363 CCACGTAGGARAGACTTGTCTCTACGCCAPAAACAATTAGCTGGCGGTGGTGGCGTGCCC 422
         ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      4668 CAACATGGCAAATCCTGTCTCTACAAAATACAAATTAGCTGGGTGATGGTGCATGC 4727

Qy      423 CTGTGGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGGATCGCTTGAGTCCGGGAGGTTGA 482
         |||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      4728 CTGTAGTCTGAGCTACTCGGGAGGCTGAGGCAGGAGGATCACTTGAGTCTGGGAGCTCAA 4787

Qy      483 GGCTGCAGTAAGCTATGACCAACGCTGCTGCACCTCCACCTGGGTGACAGAGTGAGACCTT 542
         |||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      4788 GGCTGCAGTGAGCCAAGATCATGCTACTGCACTCCAGCCTCGGCCAACACAGAGTGAGACCTT 4847

Qy      543 GTCTCAAAAAAAAAAAAAAAAAAAAAAACAAGTA 577
         |||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      4848 CTCTCAAAAAAAAAAAAAAAAAAAAAAAGCA 4882
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RESULT 12
AC084756/c

AC004756	166138 bp	DNA	linear	PRI 23-JUN-2001
LOCUS				
DEFINITION	Homo sapiens chromosome 15 clone RP11-120K9 map 15q21.2, complete sequence.			

ACCESSION	AC084756	AC027538
VERSION	AC084756.3	GI:14530845

VERSION
KEYWORDS
AC004730:3 HTG.
Homo sapiens (human)
SOURCE

SOURCE	ORGANISM
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FOR INFORMATION OF THE
 DIRECTOR, FBI, WASHINGTON, D.C.
 FROM: SAC, NEW YORK (100-100000)
 SUBJECT: [REDACTED]
 RE: [REDACTED]

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

KEYWORDS

Rowen, L., Madan, A., Kaur, S., Fleetwood, P., Burke, J., Dors, M., Pate, D. and Hood, L.

face, D. and hood, E.
Sequencing of human chromosome 15 D15S146-D15S117 region
TTTTT

INTERNATIONAL
UNPUBLISHED
DEQUALIFYING

BOOKS DISCUSSIONS

REFERENCE	2 (bases I to 100136)	Power I. Madan A. Oj
AUTHORS	Power I. Madan A. Oj	

AUTHORS
KOWEN, L., MADAN, A., QUN, S., SARAGUTAN, D., BRILL, B., BLOOM, S.,
DORS, M., DICKHOFF, R., FLEETWOOD, P., HARRISON, G., KAUR, A., MADAN,
NESBITT, R., TRACICOFF, R. and HOOD, L.

ETRE
NEDSIL, K.; IALC
N: 2004 01 01
N: 2004 01 01

LEADERS
STAFF

JOURNAL

REFERENCE 3 (pages 1 to 166138)
98105, USA
for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA

REFERENCE 3 (bases 1 to 166138)

AUTHORS

Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, K., Pate, D. and Hood, L.

TITLE	Direct Submission
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JOURNAL

for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA

COMMENT

----- Genome Center

Center: Multimegababase Sequencing Center

Center code: UWMSC

Web site: <http://chroma.mbt.washington.edu/msg> www

Contact: leerowen@systemsbiology.org

Drafting center: WIBR

----- Summary Statistics

Sequencing vector: pUC18; L08752

Chemistry: Dye-terminator Big Dye: 90% of reads

Chemistry: Dye-primer Big Dye: 10% of reads

Assembly program: Phrap; version 0.990399

Note: Data from overlapping BACs AC022403 [drafting center UWMSC], AC012170 [drafting center UWMSC], AC012100 [drafting center UWMSC], and AC010770 [drafting center WIBR] was added for finishing.

FEATURES

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/clone_lib="RPC1 human BAC library 11"
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1. .28670
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83485. .83535
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BASE COUNT 54073 a 33203 c 32122 g 46740 t
ORIGIN
Query Match 14.8%; Score 221.8; DB 9; Length 166138;
Best Local Similarity 83.0%; Pred. No. 7.6e-46;
Matches 253; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
QY 269 GGCTGGGCACGGTGGCTCAGCCCTATAATACCACTTTGGGAGGCTGAGGAGGAAGGA 328
Db 30323 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 13
AC007501/c

LOCUS	AC007501	162617 bp	DNA	linear	PRI 28-JAN-2000
DEFINITION	Homo sapiens chromosome 16 clone RPCI-11_67I13, complete sequence.				
ACCESSION	AC007501				
VERSION	AC007501.2	GI:6806839			
KEYWORDS	HTG.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
	1 (bases 1 to 162617)				
	Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Tatum, O., Campbell, C., Fawcett, J., Maltbie, M., Bussod, M., Sutherland, R., Han, C. and Deaven, L.				
AUTHORS	Sequencing of Human Chromosome 16q12				
	Unpublished				
	2 (bases 1 to 162617)				
TITLE	Ricke, D.O.				
	Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System				
	Unpublished				
JOURNAL	3 (bases 1 to 162617)				
	Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Tatum, O., Campbell, C., Fawcett, J., Maltbie, M., Bussod, M., Sutherland, R., McMurry, K., Han, C. and Deaven, L.				
	Direct Submission				
JOURNAL	Submitted (06-MAY-1999) Center for Human Genome Studies, DOE Joint Genome Institute, Los Alamos National Laboratory, MS M888, Los Alamos, NM 87545, USA				
	4 (bases 1 to 162617)				
	Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Tatum, O., Campbell, C., Fawcett, J., Maltbie, M., Bussod, M., Sutherland, R., McMurry, K., Han, C. and Deaven, L.				
REFERENCE	Direct Submission				
	Submitted (28-JAN-2000) Center for Human Genome Studies, DOE Joint Genome Institute, Los Alamos National Laboratory, MS M888, Los Alamos, NM 87545, USA				
	On Jan 28, 2000 this sequence version replaced gi:4755165.				
COMMENT	Location/Qualifiers				
FEATURES	source				
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	/organism="Homo sapiens"				
repeat_region	/mol_type="genomic DNA"				
	/db_xref="taxon:9606"				
repeat_region	/chromosome="16"				
	/clone="RPCI-11_67I13"				
repeat_region	/note="overlaps RPCI-11_132F7 and RPCI-11_142G1"				
	2201. .2311				
repeat_region	/rpt_family="MSTC"				
	2600. .8727				
repeat_region	/rpt_family="L1"				
	3933. .4186				
repeat_region	/rpt_family="MER25"				
	9067. .9178				
repeat_region	/rpt_family="Alu"				
	complement(9295. .9406)				
repeat_region	/rpt_family="HSATI"				
	9319. .9424				
repeat_region	/rpt_family="HSATI"				
	complement(9975. .10143)				
repeat_region	/rpt_family="HSATI"				
	complement(10170. .10450)				
repeat_region	/rpt_family="Alu"				
	13723. .14353				
repeat_region	/rpt_family="L1"				
	15420. .15715				
repeat_region	/rpt_family="Alu"				
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repeat_region	/rpt_family="L1"				


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repeat_region 18740. .19059
/rpt_family="Alu"
misc_feature complement(21897. .21993)
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repeat_region complement(26970. .27361)
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repeat_region 28102. .28205
/rpt_family="HERVL"
repeat_region 28484. .29764
/rpt_family="MLT2B2"
repeat_region 28837. .29143
/rpt_family="MLT"
repeat_region 29027. .29674
/rpt_family="MSTAR"
repeat_region 29059. .29124
/rpt_family="THR"
repeat_region 29163. .29644
/rpt_family="MLT"
repeat_region 29445. .29512
/rpt_family="MLR"
repeat_region 29868. .29938
/rpt_family="MSTAR"
repeat_region 30256. .30352
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repeat_region 30555. .30908
/rpt_family="MLT1"
repeat_region 34887. .35200
/rpt_family="TIGGER"
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misc_feature complement(41862. .41966)
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/rpt_family="THE1"
repeat_region complement(42177. .42339)
/rpt_family="MSTA"
repeat_region complement(42492. .42589)
/rpt_family="MST"
misc_feature 48395. .48565
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repeat_region 48908. .49210
/rpt_family="Alu"
repeat_region complement(49684. .49841)
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/rpt_family="L1"
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repeat_region complement(50515. .50737)
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repeat_region 50721. .51046
/rpt_family="Alu"
repeat_region complement(51042. .51159)
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repeat_region complement(53340. .53495)
/rpt_family="MER20"
repeat_region 57045. .57361
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repeat_region complement(57046. .57363)
/rpt_family="MER7"
repeat_region complement(57662. .58024)
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repeat_region 58654. .59663
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63652. .64081
/rpt_family="L1"
repeat_region complement(64180. .64502)
/rpt_family="Alu"
repeat_region complement(66751. .67110)
/rpt_family="THE1"
71122. .71412
/rpt_family="Alu"
repeat_region complement(73459. .73693)
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77727. .77878
/rpt_family="MER5"
78600. .78688
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82830. .83127
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/rpt_family="L1"
95753. .95889
/rpt_family="L1"
repeat_region complement(100721. .101019)
/rpt_family="Alu"
misc_feature complement(103265. .103365)
/note="GRAIL 2 excellent exon, frame 2"
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113458. .113541,115201. .115353))
/note="Homo sapiens CAGF9 mRNA, partial cds. (U80736)"
108755. .108820
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/rpt_family="Alu"
repeat_region 110274. .110343
/rpt_family="MIR"
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repeat_region 121698. .121867
/rpt_family="L1"
repeat_region complement(122342. .122660)
/rpt_family="Alu"
misc_feature complement(123676. .123705)
/note="GRAIL 2 excellent exon, frame 1"
repeat_region complement(124424. .124603)
/rpt_family="MER20"
misc_feature 127460. .127579
/note="GRAIL 2 excellent exon, frame 0"
repeat_region 128209. .128511
/rpt_family="Alu"
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Query Match 14.7%; Score 220; DB 9; Length 162617;
Best Local Similarity 73.4%; Pred.No. 2.2e-45;
Matches 295; Conservative 0; Mismatches 105; Indels 2; Gaps 1;

QY 236 GCCTGAGCTGCTGGGATTAAATCAACAGCTGTGGCTGGGCACGGTGGCTCAGCCCTATA 295
Db |||||
160154 GCCTTGGCATACTGTGTTAAAAATCACATCTTAGGCCAGGTGTGGTAGCTTACAACTGTC 160095
QY 296 ATACCAGCACTTTGGGAGGCTGAGGAGGAAGGATTGCTTGAGGCCAGAAAGTTTGAGACCA 355
Db |||||
160094 ATCTTGGCATTTTGGGAGGCTGAGGTGGTGGATCGCTTGAGCCAGAAAGTTTGAGACCA 160035
QY 356 GCCTGGGCCACGTAGGAACACCTTGTCTCTACGCACA--AACAAATTAGCTGGCGTGGT 413
Db |||||
160034 GCCTGGGCAACATAGAGAAACCTTGTCTCTACAAAAATAAAAAATTAGCTGGGTGTGAT 159975
QY 414 GCGTGCCCCCTGTGGTCCAGCTACTCAGGAGGCTGAGGCAGGAGGATCGCTTGAGTCCG 473
Db |||||
```


COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L28118
Center clone name: 2021_O_4

* NOTE: This record contains 74 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 543: contig of 543 bp in length
544 643: gap of 100 bp
644 1355: contig of 712 bp in length
1356 1455: gap of 100 bp
1456 2155: contig of 700 bp in length
2156 2255: gap of 100 bp
2256 2929: contig of 674 bp in length
2930 3029: gap of 100 bp
3030 3732: contig of 703 bp in length
3733 3832: gap of 100 bp
3833 4544: contig of 712 bp in length
4545 4644: gap of 100 bp
4645 5323: contig of 679 bp in length
5324 5423: gap of 100 bp
5424 6126: contig of 703 bp in length
6127 6226: gap of 100 bp
6227 6956: contig of 730 bp in length
6957 7056: gap of 100 bp
7057 7701: contig of 645 bp in length
7702 7801: gap of 100 bp
7802 8504: contig of 703 bp in length
8505 8604: gap of 100 bp
8605 9320: contig of 716 bp in length
9321 9420: gap of 100 bp
9421 10129: contig of 709 bp in length
10130 10229: gap of 100 bp
10230 10947: contig of 718 bp in length
10948 11047: gap of 100 bp
11048 11754: contig of 707 bp in length
11755 11854: gap of 100 bp
11855 12574: contig of 720 bp in length
12575 12674: gap of 100 bp
12675 13396: contig of 722 bp in length
13397 13496: gap of 100 bp
13497 14203: contig of 707 bp in length
14204 14303: gap of 100 bp
14304 15016: contig of 713 bp in length
15017 15116: gap of 100 bp
15117 15821: contig of 705 bp in length
15822 15921: gap of 100 bp
15922 16642: contig of 721 bp in length
16643 16742: gap of 100 bp
16743 17459: contig of 717 bp in length
17460 17559: gap of 100 bp
17560 18265: contig of 706 bp in length
18266 18365: gap of 100 bp
18366 19072: contig of 707 bp in length
19073 19172: gap of 100 bp
19173 19875: contig of 703 bp in length

19876 19975: gap of 100 bp
19976 20698: contig of 723 bp in length
20699 20798: gap of 100 bp
20799 21495: contig of 697 bp in length
21496 21595: gap of 100 bp
21596 22309: contig of 714 bp in length
22310 22409: gap of 100 bp
22410 23103: contig of 694 bp in length
23104 23203: gap of 100 bp
23204 23928: contig of 725 bp in length
23929 24028: gap of 100 bp
24029 24739: contig of 711 bp in length
24740 24839: gap of 100 bp
24840 25548: contig of 709 bp in length
25549 25648: gap of 100 bp
25649 26353: contig of 705 bp in length
26354 26453: gap of 100 bp
26454 27157: contig of 704 bp in length
27158 27257: gap of 100 bp
27258 27983: contig of 726 bp in length
27984 28083: gap of 100 bp
28084 28817: contig of 734 bp in length
28818 28917: gap of 100 bp
28919 29634: contig of 717 bp in length
29635 29734: gap of 100 bp
29735 30463: contig of 729 bp in length
30464 30563: gap of 100 bp
30564 31297: contig of 734 bp in length
31298 31397: gap of 100 bp
31398 32097: contig of 700 bp in length
32098 32197: gap of 100 bp
32198 32903: contig of 706 bp in length
32904 33003: gap of 100 bp
33004 33716: contig of 713 bp in length
33717 33816: gap of 100 bp
33817 34531: contig of 715 bp in length
34532 34631: gap of 100 bp
34632 35356: contig of 725 bp in length
35357 35456: gap of 100 bp
35457 36140: contig of 684 bp in length
36141 36240: gap of 100 bp
36241 36947: contig of 707 bp in length
36948 37047: gap of 100 bp
37048 37766: contig of 719 bp in length
37767 37866: gap of 100 bp
37867 38565: contig of 699 bp in length
38566 38665: gap of 100 bp
38666 39380: contig of 715 bp in length
39381 39480: gap of 100 bp
39481 40180: contig of 700 bp in length
40181 40280: gap of 100 bp
40281 40985: contig of 705 bp in length
40986 41085: gap of 100 bp
41086 41807: contig of 722 bp in length
41808 41907: gap of 100 bp
41908 42621: contig of 714 bp in length
42622 42721: gap of 100 bp
42722 43440: contig of 719 bp in length
43441 43540: gap of 100 bp
43541 44263: contig of 723 bp in length
44264 44363: gap of 100 bp
44364 45087: contig of 724 bp in length
45088 45187: gap of 100 bp
45188 45887: contig of 700 bp in length
45888 45987: gap of 100 bp
45989 46704: contig of 717 bp in length
46705 46804: gap of 100 bp
46805 47503: contig of 699 bp in length
47504 47603: gap of 100 bp
47604 48312: contig of 709 bp in length
48313 48412: gap of 100 bp
48413 49127: contig of 715 bp in length
49128 49227: gap of 100 bp

*	49228	49934: contig of 707 bp in length	
*	49935	50034: gap of 100 bp	
*	50035	50749: contig of 715 bp in length	
*	50750	50849: gap of 100 bp	
*	50850	51553: contig of 704 bp in length	
*	51554	51653: gap of 100 bp	
*	51654	52359: contig of 706 bp in length	
*	52360	52459: gap of 100 bp	
*	52460	53166: contig of 707 bp in length	
*	53167	53266: gap of 100 bp	
*	53267	53958: contig of 692 bp in length	
*	53959	54058: gap of 100 bp	
*	54059	54778: contig of 720 bp in length	
*	54779	54878: gap of 100 bp	
*	54879	55599: contig of 721 bp in length	
*	55600	55699: gap of 100 bp	
*	55700	56400: contig of 701 bp in length	
*	56401	56500: gap of 100 bp	
*	56501	57195: contig of 695 bp in length	
Query Match			
		14.6%; Score 219.2; DB 2; Length 59634;	
		Best Local Similarity 77.5%;	
		Pred. No. 3.1e-45;	
		Matches 279; Conservative 0; Mismatches 78; Indels 3; Gaps 1;	
QY	218	GAGGCTTCACTGTTGGAGCCTGAGCTGCTGGGATTAAATCAACAGCTGTGGCTGGGCA	277
Db	10264	GAGAGTGCCAGCTTCTGCCAAGACTCCTAAGAAAGAAATTGGGTTGGTGCGCGGCG	10323
QY	278	CGGTGGCTCACGCCTATAATACCAAGCACTTTGGGAGGCTGAGGAGGAAGGATTGCTTGAG	337
Db	10324	CGGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCTGAAGGGGAAGATGGCTTGAG	10383
QY	338	GCCAGAAGTTTGAGACCAGCCTGGGCCACGTAGGAAGACCTGTCTCTACGCACAA---A	394
Db	10384	CCCAGGAGTTTGAGATCAGCCTGGSCAACATGGCAAAACCCTGTCTCTACGAAAAATACA	10443
QY	395	CAAAATTAGCTGGGCGTGGTGGCGTGCCCTGTGGTCCCAGCTACTCAGGAGGCTGAGGCA	454
Db	10444	AAACTTAGCTGGGCACGGTGGCATGTGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGTG	10503
QY	455	GGAGGATCGCTTGAGTCCGGGAGGTTGAGGCTGCAGTAAGCTATGACCACGCTGCTGCAC	514
Db	10504	GGAGGATCACTTGAGCTGGGAGGTCGAGGCTGCAGTGAGCTATGATTACACCACCTGCAC	10563
QY	515	TCCACCCTGGGTGACAGAGTGAGACCCCTGTCTCAAAAAAAAAAAAAAAAAAAACAA	574
Db	10564	TCCAGCCAGGGTGACACAGTGAGACCCCTATCTCAAAAAAAAAATAAAAAAAAAA	10623

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